

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 12, 2005, 06:38:28 ; Search time 184 Seconds

(without alignments)

1760.776 Million cell updates/sec

Title: US-09-508-832-10

Perfect score: 1065

Sequence: 1 MAKQPSDVSECDREGRLQ.....PRMVLRLRLRYVRLVWRMH 198

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DBS=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBACKLOG=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713	66.9	44479	4	US-09-949-016-17176
2	695	65.4	417	4	US-09-949-016-5434
3	332.5	31.2	477	4	US-09-621-976-2099
4	323	30.3	398	4	US-09-621-976-2153
5	192	18.0	601	4	US-09-949-016-189929
c	125.5	11.8	1158	4	US-09-252-991A-10541
7	125.5	11.8	1455	4	US-09-252-991A-10325
c	125.5	11.8	2130	4	US-09-252-991A-10734
c	120.5	11.3	3433	4	US-09-902-540-5810
c	120.5	11.3	3434	4	US-09-902-540-564
c	119.5	11.2	26314	4	US-09-949-016-16389
c	119.5	11.2	29927	4	US-09-949-016-11814

c	13	119.5	11.2	29927	4	US-09-949-016-17474	Sequence 17474, A
c	14	119.5	11.2	29927	4	US-09-949-016-17475	Sequence 17475, A
c	15	119.5	11.2	37802	4	US-09-949-016-12639	Sequence 12639, A
c	16	118.5	11.1	1167	4	US-09-902-540-3048	Sequence 3048, Ap
c	17	118.5	11.1	5895	4	US-09-902-540-792	Sequence 792, App
c	18	118.5	10.8	2553	4	US-09-902-540-2867	Sequence 2867, Ap
c	19	115.5	10.8	17592	4	US-09-902-540-1138	Sequence 1138, Ap
c	20	114	10.7	483	4	US-09-252-991A-10520	Sequence 10520, A
c	21	114	10.7	22123	4	US-09-949-016-12376	Sequence 12376, A
c	22	114	10.7	22124	4	US-09-949-016-14666	Sequence 14666, A
c	23	113	10.6	15789	4	US-09-902-540-1139	Sequence 1139, Ap
c	24	112	10.5	3492	4	US-09-902-540-3089	Sequence 1089, Ap
c	25	111.5	10.5	2258	4	US-09-016-434-1415	Sequence 1415, Ap
c	26	111.5	10.5	3705	2	US-08-474-379C-64	Sequence 64, Appl
c	27	111.5	10.5	3705	3	US-09-146-249A-64	Sequence 64, Appl
c	28	111.5	10.5	3705	3	US-08-206-188B-64	Sequence 64, Appl
c	29	111.5	10.5	3705	4	US-09-917-254-42	Sequence 42, Appl
c	30	111.5	10.5	6825	4	US-09-949-016-13534	Sequence 13534, A
c	31	111.5	10.5	17654	4	US-09-902-540-1161	Sequence 1161, Ap
c	32	111	10.4	601	4	US-09-949-016-38645	Sequence 38645, A
c	33	111	10.4	1981	4	US-09-949-016-1058	Sequence 1058, Ap
c	34	111	10.4	8521	4	US-09-949-016-12800	Sequence 12800, A
c	35	111	10.4	13117	4	US-09-949-016-15804	Sequence 15804, A
c	36	111	10.4	32010	4	US-09-949-016-13127	Sequence 13127, A
c	37	110.5	10.4	24459	4	US-09-902-540-5004	Sequence 5004, Ap
c	38	110.5	10.4	32241	4	US-09-902-540-1247	Sequence 1247, Ap
c	39	110	10.3	35784	4	US-09-949-016-16785	Sequence 16785, A
c	40	110	10.3	35784	4	US-09-949-016-16786	Sequence 16786, A
c	41	109.5	10.3	47476	4	US-09-949-016-12179	Sequence 12179, A
c	42	109.5	10.3	47476	4	US-09-949-016-14472	Sequence 14472, A
c	43	109	10.2	1419	4	US-09-902-540-5186	Sequence 5186, Ap
c	44	109	10.2	11854	4	US-09-902-540-1037	Sequence 1037, Ap
c	45	109	10.2	34094	4	US-09-292-034-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-17176
; Sequence 17176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17176
; LENGTH: 44479
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(44479)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17176

Alignment Scores:
Pred. No.: 8,93e-53
Score: 713.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 66.95%
DB: 4
Length: 44479
Matches: 131
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-508-832-10 (1-198) x US-09-949-016-17176 (1-44479)

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Qy 1 MetAlaIysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 2001 ATGGCAAAGCAACCTTCTGATGTAAGTCTGAGTGTGACCGAGAAGGTAGACAATTGCAG 2060
Qy 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 2061 CCTCGGAGAGGCTCCCACTCAGACCTGGGGCCCTACTCTCCCTACACAGAGCCA 2120
Qy 41 GlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPro 60
Db 2121 CAAGGTAATCTGAAGCAATCACGGAGGTGAAGGGACAGCTGCCCCACGGCAGCCCT 2180
Qy 61 GlnGlyProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 2181 CAGGGCCGCTGGGCCCACTCCAGCCAGCCCTGGCCCTTTTGTACAGATCCCGCTTTTC 2240
Qy 81 IlePheMetArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPheAsp 100
Db 2241 ATCTTTATGAGAAATCTCCCTGCTGCTCGATCTCCAGTGGGTATTTCTCTTTTGAC 2300
Qy 101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProPro 120
Db 2301 ACAGCAGGAGCCCGACCCATCATGTTGTGACAAATCAACACAAACCCCAAGTCTCTCT 2360
Qy 121 CysGlnAlaPheAsnHisTyrLeuSerAlaMet 131
Db 2361 TGCCAGGCTTCAACCACTATCTCAGTGCATG 2393
```

RESULT 2

US-09-949-016-5434
; Sequence 5434, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5434
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5434

Alignment Scores:
Pred. No.: 5,01e-54 Length: 417
Score: 596.00 Matches: 138
Percent Similarity: 69.70% Conservative: 0
Best Local Similarity: 69.70% Mismatches: 0
Query Match: 65.35% Indels: 60
DB: 4 Gaps: 1

US-09-508-832-10 (1-198) x US-09-949-016-5434 (1-417)

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Qy 1 MetAlaIysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 1 ATGGCAAAGCAACCTTCTGATGTAAGTCTGAGTGTGACCGAGAAGGTAGACAATTGCAG 60
Qy 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 61 CCTCGGAGAGGCTCCCACTCAGACCTGGGGCCCTACTCTCCCTACACAGAGCCA 120
```

```
Qy 41 GlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPro 60
Db 121 CAA----- 123
Qy 61 GlnGlyProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 123 ----- 123
Qy 81 IlePheMetArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPheAsp 100
Db 123 ----- 123
Qy 101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProPro 120
Db 124 ---GACAGGAGCCCGACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTCT 180
Qy 121 CysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAla 140
Db 181 TGCCAGGCTTCAACCACTATCTCAGTGCATGCGTTCATGAGGCAAGGCTGAACCTGCA 240
Qy 141 AspMetArgProGluLulleTrrPleAlaGlnGluLeuArgArglleGlyAspGluPheAsn 160
Db 241 GATATGCGCCCGACAGATATGATCGCCCAAGAGTTGCGGCGTATCGGAGACGAGTTTAA 300
Qy 161 AlaTyrTyrAlaArgArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArg 180
Db 301 GCTTACTATGCAAGGAGGGTATTTTGAATAATATACCAAGCAGCCGAAGACCCACGCA 360
Qy 181 MetValIleLeuArgLeuLeuArgTyrIleValArgLeuValTyrArgMetHis 198
Db 361 ATGGTTATCTTACGACTGTACGTTACGTTGCGCTCGCTGGTGGAGAATGCAT 414
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RESULT 3

US-09-621-976-2099
; Sequence 2099, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2099
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 223..372
US-09-621-976-2099

Alignment Scores:
Pred. No.: 2,87e-21 Length: 477
Score: 332.50 Matches: 76
Percent Similarity: 48.12% Conservative: 1
Best Local Similarity: 47.50% Mismatches: 5
Query Match: 31.22% Indels: 78
DB: 4 Gaps: 2

US-09-508-832-10 (1-198) x US-09-621-976-2099 (1-477)

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Qy 1 MetAlaIysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGln-LeuGln 20
Db 223 ATGGCAAAGCAACCTTCTGATGTAAGTCTGAGTGTGACCGAGAAGGTAGACAATTGCA 282
Qy 20 nProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPr 40
Db 283 GCCTGCGAGAGGCGCTCCCACTCAGACCTGGGGCCCTACTCTCCCTACACAGAGGCC 342
```

QY 40 oGlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPr 60
Db 343 ACNA----- 346
QY 60 oGlnGlyProLeuAlaProAlaSerProGlyProPheAlaThrArgSerProLeuPh 80
Db 346----- 346
QY 80 ellePheMetArgArgSerSerLeuLeuSerArgSerSerGlyTyrrPheSerPheAs 100
Db 346----- 346
QY 100 pThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProPr 120
Db 347 ----GACAGAGCCAGCAGCCCATGAGTTGTGCAAAATCAACACAAACCCCAAGTCTCTC 402
QY 120 oCysGlnAlaPheAsnHisTyrrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAl 140
Db 403 TTGCCAGGCCCTTCAACCACTATCTCAGTGCATGTAGTCATC----- 445
QY 140 aAspMetArgProGluLeuTrpIleAlaGlnGluLeuArgArgIleGlyAspGluPhe 159
Db 446 -----CTAGAGGATATAGGTGATCTTTTC 469

RESULT 4

US-09-621-976-2153
; Sequence 2153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2153
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 18..239
; NAME/KEY: misc_feature
; LOCATION: 14
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-2153

Alignment Scores:
Pred. No.: 1.6e-20 Length: 398
Score: 323.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.33% Indels: 0
DB: 4 Gaps: 0

US-09-508-832-10 (1-198) x US-09-621-976-2153 (1-398)

QY 1 MetAlaLysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 223 ATGCAAGCAACCTTCTGATGTAAAGTTCTGAGTGTGACCGAGAGAGGTAGACAATTGCAG 282
QY 21 ProAlaGluArgProProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 283 CTTGCGGAGAGGGCTCCAGCTCAGACCTGGGGCCCTACCTCCCTACACAGACAGACCA 342
QY 41 GlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGly 58
Db 343 CAAGGTAAATCTTGAAGCAATACCGGAGGTGAAGGGGACAGCTGCCCCCAGCGC 396

RESULT 5

US-09-949-016-189929
; Sequence 189929, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189929
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189929

Alignment Scores:
Pred. No.: 1.68e-08 Length: 601
Score: 192.00 Matches: 37
Percent Similarity: 90.70% Conservative: 2
Best Local Similarity: 86.05% Mismatches: 4
Query Match: 18.03% Indels: 0
DB: 4 Gaps: 0

US-09-508-832-10 (1-198) x US-09-949-016-189929 (1-601)

QY 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluIle 146
Db 215 TTTTGTCTGTGATGCAGCTTCCATGAGCGCAGGCTGAACCTGCAGATATGCCCCAGAGATA 274
QY 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrrAlaAspArg 166
Db 275 TGGATCGCCCAAGATTGCGCGTATYGAGACGAGTTTAACCTTACTATGCAAGGAGG 334
QY 167 ValPheLeu 169
Db 335 GTAATGATG 343

RESULT 6

US-09-252-991A-10541/c
; Sequence 10541, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10541
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10541

Alignment Scores:
Pred. No.: 0.0393 Length: 1158
Score: 125.50 Matches: 55
Percent Similarity: 37.10% Conservative: 14

Best Local Similarity: 29.57% Mismatches: 67
 Query Match: 11.78% Indels: 50
 DB: 4 Gaps: 9

US-09-508-832-10 (1-198) x US-09-252-991A-10541 (1-1158)

Qy 21 ProAlaGluArgProGlnLeuArgProGly-----AlaProThrSerLeuGln 37
 Db 814 CCTCGACGAAAGCGCGCGCCGAGCCAGGCGCTGCGTCCGCGCAGGTGCGCC 755
 Qy 38 ThrGluProGlnGly-----AsnProGluGlyAsnHis-----Gly 49
 Db 754 AGCGTCCAGTGGCGCGCTGGAATGCCCTCCAGGAGCCATCGGCCGCGCCCGC 695
 Qy 50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProAlaSer 69
 Db 694 GGGTCAGGCTCCAGCGCAACTCCAGGTTTCGGGTGGCGCGCCAGCGCTCCAGTCCG 635
 Qy 70 ProGlyProPheAlaThrArgSerProLeuPhePheMetArgArgSerSerLeuLeu 89
 Db 634 CGAGCCAGGCGCGTGGCCGGATGAC-----GGACGTAGTCAGCCACA 590
 Qy 90 SerArgSerSerGlyTyrPheSerPheAspThrAsp---ArgSerProAlaProMet 108
 Db 589 GCACGG-----GACCGGATAGCGTTCTCCAGCGCCTCGC 554
 Qy 109 Ser-----CysAspIysSerThrGlnThrProSerPro 119
 Db 553 GGAGCAGCGCGAGCAAGGCGTCTAGCGCGTGGCGGCGCAGCAGCGCCTCGG 494
 Qy 120 ProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluPro 139
 Db 493 CCTGCATCGGCGCAGCAGATCGCTTCGGCGGTTGCAACTCGACACGCTGGCGCGCCG 434
 Qy 140 AlaAspMetArgProGluIleTyrPheAlaGlnGluLeuArgGlyAspGluPhe 159
 Db 433 CCAGGTGTCGCACAACC----- 416
 Qy 160 AsnAlaTyrTyrAlaArg-ArgValPheLeuAsn---AsnTyrGlnAlaAlaGluAspHi 178
 Db 415 AGGCGAGAGAGAGCGCGCTCGCGGTGAGCTTGACGGCGATTTCAGCGCGCTCGCCGACCA 356
 Qy 178 sProArgMetValIle 183
 Db 355 CCCGGGTGAGCTGTA 340

RESULT 7

US-09-252-991A-10325
 ; Sequence 10325, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 10325
 ; LENGTH: 1455
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-10325

Alignment Scores:
 Pred. No.: 0.0538 Length: 1455
 Score: 125.50 Matches: 55
 Percent Similarity: 37.10% Conservative: 14
 Best Local Similarity: 29.57% Mismatches: 67

Query Match: 11.78% Indels: 50
 DB: 4 Gaps: 9

US-09-508-832-10 (1-198) x US-09-252-991A-10325 (1-1455)

Qy 21 ProAlaGluArgProGlnLeuArgProGly-----AlaProThrSerLeuGln 37
 Db 624 CCTCGACGAAAGCGCGCGCCGAGCCAGGCGCTGCGTCCGCGCAGGTGCGCC 683
 Qy 38 ThrGluProGlnGly-----AsnProGluGlyAsnHis-----Gly 49
 Db 684 AGCGTCCAGTGGCGCGCTGGAATGCCCTCCAGGAGCCATCGGCCGCGCCCGC 743
 Qy 50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProAlaSer 69
 Db 744 GGGTCAGGCTCCAGCGCAACTCCAGGTTTCGGGTGGCGCGCCAGCGCTCCAGTCCG 803
 Qy 70 ProGlyProPheAlaThrArgSerProLeuPhePheMetArgArgSerSerLeuLeu 89
 Db 804 CGAGCCAGGCGCGTGGCCGGATGAC-----GGACGTAGTCAGCCACA 848
 Qy 90 SerArgSerSerGlyTyrPheSerPheAspThrAsp---ArgSerProAlaProMet 108
 Db 849 GCACGG-----GACCGGATAGCGTTCTCCAGCGCCTCGC 884
 Qy 109 Ser-----CysAspIysSerThrGlnThrProSerPro 119
 Db 885 GGAGCAGCGCGAGCAAGGCGTCTAGCGCGTGGCGGCGCAGCAGCGCCTCGG 944
 Qy 120 ProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluPro 139
 Db 945 CCTGCATCGGCGCAGCAGATCGCTTCGGCGGTTGCAACTCGACACGCTGGCGCGCCG 1004
 Qy 140 AlaAspMetArgProGluIleTyrPheAlaGlnGluLeuArgGlyAspGluPhe 159
 Db 1005 CCAGGTGTCGCACAACC----- 1022
 Qy 160 AsnAlaTyrTyrAlaArg-ArgValPheLeuAsn---AsnTyrGlnAlaAlaGluAspHi 178
 Db 1023 AGGCGAGAGAGAGCGCGCTCGCGGTGAGCTTGACGGCGATTTCAGCGCGCTCGCCGACCA 1082
 Qy 178 sProArgMetValIle 183
 Db 1083 CCCGGGTGAGCTGTA 1098

RESULT 8

US-09-252-991A-10734/c
 ; Sequence 10734, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 10734
 ; LENGTH: 2130
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-10734

Alignment Scores:
 Pred. No.: 0.0906 Length: 2130
 Score: 125.50 Matches: 55
 Percent Similarity: 37.10% Conservative: 14
 Best Local Similarity: 29.57% Mismatches: 67
 Query Match: 11.78% Indels: 50

[illegible]

US-09-508-832-10 (1-198) x US-09-949-016-11814 (1-29927)

Qy	9	SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgPro	26
		:::	
Db	20801	TCCCCAAGCCTCTCCCGGACACCAAGGTGTCCAAGCTCTCCGGGTCA	20742
		:::	
Qy	27	GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnG	42
		:::	
Db	20741	AGGCTCTCTCCCGAGACACCAAGGTCCCCCAGCCTCTCCCGAGGACAC	20682
		:::	
Qy	42	YasnProGlu-----GlyAsnHisGlyGlyG	51
		:::	
Db	20681	CTCTCCCGAGACACCAAGGTCCCCAAGCCTCTCCCGGACACCAAGGT	20622
		:::	
Qy	51	uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaPro	69
		:::	
Db	20621	CGGTCCTACTAGTCCCCCAAGGCACCTCCGAGACACCAAGGTCCCCA	20562
		:::	
Qy	69	rProGlyProPheAla-----ThrArgSerProLeuPheIlePheMetArg	85
		:::	
Db	20561	ACCAGGTCCCGAAGGCTCTCCCGAGGACACCAAGTCCCCAAGGTCTC	20502
		:::	
Qy	85	gSerSerLeuLeuSerArg---SerSerSerGlyTyrPheSerPheAspThr	101
		:::	
Db	20501	GTCCCCAGGCCTCTCCAGGTTCACAGGTCCCCAAGCCTCTCTCGGAC	20442
		:::	
Qy	102	-----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThr	117
		:::	
Db	20441	AAGCCTCTCCCGGACACCAAGTCCCAAGCC-----TCTCCGGGACAC	20391
		:::	
Qy	118	-----SerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMet	132
		:::	
Db	20390	CCCAAGCCTCTCCCGCTCACCAGATCTCCAAGCCTCTCCAGGACACCA	20331
		:::	
Qy	132	laSerMetArg-----GlnAlaGluProAlaAspMetArg	143
		:::	
Db	20330	CTCTCCCCAGGACACCAAGTCCCCAAGCCTCTCTCCCGAGGACACCA	20284
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RESULT 13

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US-09-949-016-17474/C
; Sequence 17474, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17474
; LENGTH: 29927
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(29927)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17474

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Alignment Scores:		
Pred. No.:	11.7	Length: 29927
Score:	119.50	Matches: 60
Percent Similarity:	41.24%	Conservative: 13
Best Local Similarity:	33.90%	Mismatches: 59
Query Match:	11.22%	Indels: 45

DB:	4	Gaps:	11
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US-09-508-832-10 (1-198) x US-09-949-016-17474 (1-29927)

Qy 9 SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgProPro 26
Db 20801 TCCCAAGCCTCTCCCGGGACACCAAGGTGTCCAAAGCTTCTCCGGGTACCAGGTCCCCA 20742
Qy 27 GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnG1 42
Db 20741 AGGCTCTCTCCGAGACACCAAGTCCCCAGCTCTCCCCAGGACACCAAGATCCCCAAGG 20682
Qy 42 VAsnProGlu-----GlyAsnHisGlyGlyG1 51
Db 20681 CTCTCCCAAGGACACCAAGTCCCCAAGCTTCTCCCGGGACACCAAGTCCCCAAGCCTCTCC 20622
Qy 51 uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaProAlaase 69
Db 20621 CGGGTCACTAGTCTCCCAAGGCATCTCCGAGACACCAAGTCTCCCAAGCTCTCCAGGTC 20562
Qy 69 rProGlyProPheAla-----ThrArgSerProLeuPhePheMetArgAr 85
Db 20561 ACCAGTCCCCAAGGCTCTCCCAAGGACACCAAGTCCCCAAGGCTCTCCGGGTACCAG 20502
Qy 85 gSerSerLeuLeuSerArg---SerSerSerGlyTyzrPheSerPheAspThr----- 101
Db 20501 GTCCCAAGCCTCTCAAGGTCCCAAGTCCCAAGCCTCTCTCTGGGACACCAAGGTGTCC 20442
Qy 102 -----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThrPro--- 117
Db 20441 AAGCTTCTCCCGGGACACCAAGTCCCCAAGCC-----TCTCCGGGACACCAAGTCT 20391
Qy 118 -----SerProProCysGlnAlaPheAsnHisTyzrLeuSerAlaMetA 132
Db 20390 CCCAAGCCTCTCCGGTCTCACAGATCTCCAAGCTCTCCCAAGGACACCAAGTCCCCAAG 20331
Qy 132 laSerMetArg-----GlnAlaGluProAlaAspMetArg 143
Db 20330 CTCTCCCAAGGACACCAAGTCCCCAAGCCTCTCTCCCAAGGACACCAAGG 20284

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RESULT 14

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US-09-949-016-17475/c
; Sequence 17475, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17475
; LENGTH: 29927
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(29927)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17475

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Alignment Scores:		
Pred. No.:	11.7	29327
Score:	119.50	Length:
Percent Similarity:	41.24%	Matches: 60
		Conservative: 13

Best Local Similarity: 33.90% Mismatches: 59
Query Match: 11.22% Indels: 45
DB: 4 Gaps: 11
US-09-508-832-10 (1-198) x US-09-949-016-17475 (1-29927)

Qy 9 SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgProPro 26
Db 20801 TCCCAAGCCTCTCCCGGACACCAAGGTGTCCAAGCCTCTCCCGGGTCCACCAAGTCCCCA 20742
Qy 27 GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnG1 42
Db 20741 AGGCTCTCTCCGAGACACCAAGTGTCCCAAGCCTCTCCCGAGACACCAAGTCCCCAAGG 20682
Qy 42 YAsnProGlu-----GlyAsnHisGlyGlyG1 51
Db 20681 CTCTCCGAGACACCAAGTGTCCCAAGCCTCTCCCGGACACCAAGTGTCCCAAGCCTCTCC 20622
Qy 51 uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaProAlaSe 69
Db 20621 CGGGTCACTAGGTCTCCCAAGGCACTCCCGAGACACCAAGTGTCCCAAGCCTCTCCAAGGTC 20562
Qy 69 rProGlyProPheAla-----ThrArgSerProLeuPheIlePheMetArgAr 85
Db 20561 ACCAGGTCTCCCAAGGCTCTCCCGAGACACCAAGTGTCCCAAGCCTCTCCCGGGTCCACCAG 20502
Qy 85 gSerSerLeuLeuSerArg---SerSerSerGlyTyPheSerPheAspThr----- 101
Db 20501 GTCCCAAGCCTCTCCAAGGTCAACAGGTCTCCCAAGCCTCTCTCTGGGACACCAAGGTGTCC 20442
Qy 102 -----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThrPro----- 117
Db 20441 AAGCCTCTCCCGGACACCAAGTGTCCCAAGCCTCTCCCGGACACCAAGTGTCCCAAGGTC 20391
Qy 118 -----SerProProCysGlnAlaPheAsnHisTyLeuSerAlaMeta 132
Db 20390 CCCAAGCCTCTCCCGGTCAACAGTGTCCCAAGCCTCTCCCGGACACCAAGTGTCCCAAG 20331
Qy 132 laSerMetArg-----GlnAlaGluProAlaAspMetArg 143
Db 20330 CCTCTCCGAGACACCAAGTGTCCCAAGCCTCTCCCGGACACCAAGTGTCCCAAG 20284

RESULT 15

US-09-949-016-12639/c
; Sequence 12639, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12639
; LENGTH: 37802
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(37802)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12639

Alignment Scores:

Pred. No.: 16.2 Length: 37802

Score: 119.50 Matches: 60
Percent Similarity: 41.24% Conservative: 13
Best Local Similarity: 33.90% Mismatches: 59
Query Match: 11.22% Indels: 45
DB: 4 Gaps: 11
US-09-508-832-10 (1-198) x US-09-949-016-12639 (1-37802)

Qy 9 SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgProPro 26
Db 20801 TCCCAAGCCTCTCCCGGACACCAAGGTGTCCAAGCCTCTCCCGGGTCCACCAAGTCCCCA 20742
Qy 27 GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnG1 42
Db 20741 AGGCTCTCTCCGAGACACCAAGTGTCCCAAGCCTCTCCCGAGACACCAAGTCCCCAAGG 20682
Qy 42 YAsnProGlu-----GlyAsnHisGlyGlyG1 51
Db 20681 CTCTCCGAGACACCAAGTGTCCCAAGCCTCTCCCGGACACCAAGTGTCCCAAGCCTCTCC 20622
Qy 51 uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaProAlaSe 69
Db 20621 CGGGTCACTAGGTCTCCCAAGGCACTCCCGAGACACCAAGTGTCCCAAGCCTCTCCAAGGTC 20562
Qy 69 rProGlyProPheAla-----ThrArgSerProLeuPheIlePheMetArgAr 85
Db 20561 ACCAGGTCTCCCAAGGCTCTCCCGAGACACCAAGTGTCCCAAGCCTCTCCCGGGTCCACCAG 20502
Qy 85 gSerSerLeuLeuSerArg---SerSerSerGlyTyPheSerPheAspThr----- 101
Db 20501 GTCCCAAGCCTCTCCAAGGTCAACAGGTCTCCCAAGCCTCTCTCTGGGACACCAAGGTGTCC 20442
Qy 102 -----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThrPro----- 117
Db 20441 AAGCCTCTCCCGGACACCAAGTGTCCCAAGCCTCTCCCGGACACCAAGTGTCCCAAGGTC 20391
Qy 118 -----SerProProCysGlnAlaPheAsnHisTyLeuSerAlaMeta 132
Db 20390 CCCAAGCCTCTCCCGGTCAACAGTGTCCCAAGCCTCTCCCGGACACCAAGTGTCCCAAG 20331
Qy 132 laSerMetArg-----GlnAlaGluProAlaAspMetArg 143
Db 20330 CCTCTCCGAGACACCAAGTGTCCCAAGCCTCTCCCGGACACCAAGTGTCCCAAG 20284

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	696	65.4	826	US-10-755-889-15	Sequence 15, Appl
2	560	52.6	536	US-09-918-995-31159	Sequence 31159, A
3	497	46.7	442	US-10-430-763-1154	Sequence 1154, Ap
4	437	41.0	403	US-09-918-995-36495	Sequence 36495, A
5	192	18.0	455	US-10-027-632-75254	Sequence 75254, A
6	192	18.0	455	US-10-027-632-313542	Sequence 313542, A
7	192	18.0	455	US-10-027-632-75254	Sequence 75254, A
8	192	18.0	455	US-10-027-632-313542	Sequence 313542, A
9	189.5	17.8	199	US-10-092-750-72	Sequence 72, Appl
10	178	16.7	105	US-10-092-750-153	Sequence 153, App
c 11	125.5	11.8	1101	US-10-282-122A-7256	Sequence 7256, Ap
c 12	121.5	11.4	1933	US-10-437-963-96145	Sequence 96145, A
c 13	120.5	11.3	147223	US-10-981-277-21	Sequence 21, Appl
c 14	120.5	11.3	151882	US-10-981-277-22	Sequence 22, Appl
c 15	119.5	11.2	32367	US-10-158-160A-14	Sequence 14, Appl
16	118.5	11.1	836	US-10-425-115-11764	Sequence 11764, A
17	117.5	11.0	2166	US-10-437-963-35782	Sequence 35782, A
c 18	116.5	10.9	9025608	US-10-156-761-1	Sequence 1, Appli
c 19	116	10.9	557	US-10-425-115-148175	Sequence 148175, A
c 20	116	10.9	672	US-10-767-701-13103	Sequence 13103, A
c 21	116	10.9	759	US-10-240-425-590	Sequence 590, App
c 22	115.5	10.8	862	US-10-767-701-3261	Sequence 3261, Ap
c 23	115.5	10.8	2544	US-10-369-493-43062	Sequence 43062, A
24	115	10.8	780	US-10-156-761-2892	Sequence 2892, Ap
c 25	115	10.8	125746	US-10-156-761-15102	Sequence 15102, A
c 26	115	10.8	9025608	US-10-156-761-1	Sequence 1, Appli
27	114.5	10.8	1305	US-10-156-761-3516	Sequence 3516, Ap
c 28	114	10.7	1785	US-10-437-963-92703	Sequence 92703, A
29	114	10.7	2317	US-09-764-875-294	Sequence 294, App
c 30	114	10.7	2847	US-10-437-963-89518	Sequence 89518, A
c 31	113.5	10.7	893	US-10-425-115-71067	Sequence 71067, A
c 32	113	10.6	2345	US-10-310-154-287	Sequence 287, App
33	113	10.6	2345	US-10-732-923-179	Sequence 179, App
34	112.5	10.6	1123	US-10-425-115-701	Sequence 701, App
35	112.5	10.6	2862	US-10-437-963-6992	Sequence 6992, Ap
36	112.5	10.6	3608	US-10-887-553A-633	Sequence 633, App
c 37	112	10.5	1191	US-10-437-963-58554	Sequence 58554, A
c 38	112	10.5	1958	US-10-488-056-17	Sequence 17, Appl
c 39	112	10.5	2370	US-10-450-763-20228	Sequence 20228, A
40	112	10.5	15738	US-10-329-079-12	Sequence 12, Appl
c 41	112	10.5	37360	US-10-329-079-6	Sequence 6, Appli
c 42	111.5	10.5	1116	US-10-214-446-5	Sequence 5, Appli
43	111.5	10.5	1726	US-10-645-190-3	Sequence 3, Appli
44	111.5	10.5	2258	US-09-964-824A-261	Sequence 261, App
45	111.5	10.5	2258	US-10-305-720-1415	Sequence 1415, Ap

ALIGNMENTS

RESULT 1

US-10-755-889-15
; Sequence 15, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10755.889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757

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; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patent version 3.2
; SEQ ID NO 15
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-15

Alignment Scores:
Pred. No.: 4,996-65 Length: 826
Score: 696.00 Matches: 138
Percent Similarity: 69.70% Conservative: 0
Best Local Similarity: 69.70% Mismatches: 0
Query Match: 65.35% Indels: 60
DB: 20 Gaps: 1

US-09-508-832-10 (1-198) x US-10-755-889-15 (1-826)

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Db 1 ATGGCAAGCAACCTTCTGATTAAGTCTGAGTGTGACCGAAGAGGTAGACAATTGCAG 60
QY 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 61 CTGCGGAGAGGCGCTCCCGAGCTCAGACTGGGGCCCTTACCTCCCTACAGACAGCCA 120
QY 41 GlnGlyAenProGluGlyAenHisGlyGlyGluGlyAenSerCysProHisGlySerPro 60
Db 121 CAA----- 123
QY 61 GlnGlyProLeuAlaProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 123 ----- 123
QY 81 IlePheMetArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
Db 123 ----- 123
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Db 181 TGCCAGGCGCTTCAACCACTATCTCAGTGCATGCAATGGCTTCCATGAGGAGGCTGAACCTGCA 240
QY 141 AspMetArgProGluIleTyrPheAlaGlnGluLeuArgArgIleGlyAspGluPheAen 160
Db 241 GATATGGGCCAGAGATATGGATCGCCCAAGAGTTGGCGGTATTGGAGACGAGTTTAAC 300
QY 161 AlaTyrTyrAlaArgArgValPheLeuAenAenTyrGlnAlaAlaGluAspHisProArg 180
Db 301 GCTTACTATGCAAGGAGGGTATTTTGAATAATTACCAAGCAGCGCCGAGACCCACCACCA 360
QY 181 MetValIleLeuArgLeuLeuArgTyrIleValArgLeuValTyrArgMethHis 198
Db 361 ATGGTTATCTTACGACTGTACGTATACATTTGTCGCGCTGGTGTGGAGATGCAAT 414

RESULT 2
US-09-918-995-31159
; Sequence 31159, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31159
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(536)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31159

Alignment Scores:
Pred. No.: 1,296-50 Length: 536
Score: 560.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 52.58% Indels: 0
DB: 10 Gaps: 0

US-09-508-832-10 (1-198) x US-09-918-995-31159 (1-536)

QY 1 MetAlaLysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 223 ATGGCAAGCAACCTTCTGATTAAGTCTGAGTGTGACCGAAGAGGTAGACAATTGCAG 282
QY 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 283 CTGCGGAGAGGCGCTCCCGAGCTCAGACTGGGGCCCTTACCTCCCTACAGACAGCCA 342
QY 41 GlnGlyAenProGluGlyAenHisGlyGlyGluGlyAenSerCysProHisGlySerPro 60
Db 343 CAAAGTATCTCTGAAGCAATCAGGAGGTGAAGGGGAGCAGCTGCCCGCAGCCCT 402
QY 61 GlnGlyProLeuAlaProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 403 CAGGCGCGCTGGCCCGCAGCTGCCAGCCCTGGCCCTTTTGTCTACAGATCCCGCTTTTC 462
QY 81 IlePheMetArgArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
Db 463 ATCTTTATGAGAAGATCTCTCTGCTGCTCGATCTCGATGGGTATTTCTCTTTTGAC 522
QY 101 ThrAspArgSer 104
Db 523 ACAGACAGGAGC 534

RESULT 3
US-10-450-763-1154
; Sequence 1154, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 1154
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (167)-(442)
; OTHER INFORMATION: 100% homologous to Homo sapiens BimEL, accession number
; OTHER INFORMATION: AF032457, Smith-Waterman Score=497.
US-10-450-763-1154
```

```
Alignment Scores:
Pred. No.: 6 21e-44 Length: 442
Score: 497.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.67% Indels: 0
DB: 24 Gaps: 0

US-09-508-832-10 (1-198) x US-10-450-763-1154 (1-442)

Qy 1 MetAlaYsGlnProSerAspValSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 167 ATGCCAAGCAACCTTCTGATGAAGTCTGAGTGTGACCGAGAGGAGGTAGACAATTGCAG 226
Qy 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 227 CCTCGGAGAGGCGCTCCCGACCTCAGACCTGGGGCCCTTACCTCCCTACACAGAGGCCA 286
Qy 41 GlnGlyAenProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPro 60
Db 287 CAAGTAATCTCTGAAGCAATACGGAGGTGAGGGGACAGCTGCCCGCCAGCGCCT 346
Qy 61 GlnGlyProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 347 CAGGCGCGCTGGCGCCACCTGCCAGCCTGGCCCTTTTGTACAGATCCCGCTTTC 406
Qy 81 IlePheMetArgArgSerSerLeuLeuSerArgSer 92
Db 407 ATCTTTATGAGAAGATCTCCCTGCTGTCGATCC 442

RESULT 4
US-09-918-995-36495
; Sequence 36495, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36495
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36495

Alignment Scores:
Pred. No.: 1.59e-37 Length: 403
Score: 437.00 Matches: 79
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.03% Indels: 0
DB: 10 Gaps: 0

US-09-508-832-10 (1-198) x US-09-918-995-36495 (1-403)

Qy 1 MetAlaYsGlnProSerAspValSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 167 ATGCCAAGCAACCTTCTGATGAAGTCTGAGTGTGACCGAGAGGAGGTAGACAATTGCAG 226
Qy 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 227 CCTCGGAGAGGCGCTCCCGACCTCAGACCTGGGGCCCTTACCTCCCTACACAGAGGCCA 286
Qy 41 GlnGlyAenProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPro 60
Db 287 CAAGTAATCTCTGAAGCAATACGGAGGTGAGGGGACAGCTGCCCGCCAGCGCCT 346

Alignment Scores:
Pred. No.: 4.26e-11 Length: 455
Score: 192.00 Matches: 37
Percent Similarity: 90.70% Conservative: 2
Best Local Similarity: 86.05% Mismatches: 4
Query Match: 18.03% Indels: 0
DB: 14 Gaps: 0

US-09-508-832-10 (1-198) x US-10-027-632-75254 (1-455)

Qy 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluLe 146
Db 64 TTTTGTCTGTGATGCAGCTTCCATGAGGCGAGCTGAACCTGCAGATATCGGCCAGAGATA 123
Qy 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArg 166
Db 124 TGGATCCTCCCAAGAGTTGCGCGGTATYGGAGACGAGTTTAAACGCTTACTATGCAAGGAGG 183
Qy 167 ValPheLeu 169
Db 184 GTAATGATG 192

RESULT 6
US-10-027-632-313542
; Sequence 313542, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

US-10-027-632-75254

Alignment Scores:

Pred. No.:	4.26e-11	Length:	455
Score:	192.00	Matches:	37
Percent Similarity:	90.70%	Conservative:	2
Best Local Similarity:	86.05%	Mismatches:	4
Query Match:	18.03%	Indels:	0
DB:	18	Gaps:	0

US-09-508-832-10 (1-198) x US-10-027-632-75254 (1-455)

Qy 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluile 146
 Db 64 TTTTGTCTGCATGCAGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCACAGATA 123

Qy 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArg 166
 Db 124 TGGATGCCCAAGAGTTGGCGGTATYGAGACGAGTTTAAACGCTTACTATGCAAGGAG 18

Qy 167 ValPheLeu 169
 Db 184 GTAATGATG 192

RESULT 8

US-10-027-632-313542

; Sequence 313542, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 313542

; LENGTH: 455

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-313542

Alignment Scores:

Pred. No.:	4.26e-11	Length:	455
Score:	192.00	Matches:	37
Percent Similarity:	90.70%	Conservative:	2
Best Local Similarity:	86.05%	Mismatches:	4
Query Match:	18.03%	Indels:	0
DB:	18	Gaps:	0

US-09-508-832-10 (1-198) x US-10-027-632-313542 (1-455)

Qy 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluile 146
 Db 64 TTTTGTCTGCATGCAGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCACAGATA 123

Qy 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArg 166
 Db 124 TGGATGCCCAAGAGTTGGCGGTATYGAGACGAGTTTAAACGCTTACTATGCAAGGAG 18

Qy 167 ValPheLeu 169
 Db 184 GTAATGATG 192

RESULT 7

US-10-027-632-75254

; Sequence 75254, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 75254

; LENGTH: 455

; TYPE: DNA

; ORGANISM: Human

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Db 124 TGGATCGCCCAAGAGTTGCGGCTATYGGAGACGAGTTTAAACGCTTACTATGCAAGGAGG 183
Qy 167 ValPheLeu 169
Db 184 GTAATGATG 192

RESULT 9
US-10-092-750-72
; Sequence 72, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-750-72

Alignment Scores:
Pred. No.: 2,99e-11 Length: 199
Score: 189.50 Matches: 39
Percent Similarity: 81.48% Conservativeness: 5
Best Local Similarity: 72.22% Mismatches: 5
Query Match: 17.79% Indels: 5
DB: 15 Gaps: 2

US-09-508-832-10 (1-198) x US-10-092-750-72 (1-199)
Qy 124 PheAenHisTyLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArg 143
Db 33 TACAATTCTTACTTACACA---ATGGCTTCCATGAGCGAGGCTGAACCTGCAGATATGCGC 89
Qy 144 ProGluIleTrpIleAlaGlnGluLeuArgGlyGlyAspGluPheAsnAlaTyTr 163
Db 90 CCAGAGATATGATCGCCCAAGAGTTGCGGCTATTGAGACGAGTTTAAACGCTTACTAT 149
Qy 164 AlaArgArgValPheLeuAsnAsnTyTrGlnAlaAlaGluAsp 177
Db 150 GCAAGG-----GAGGATTACAAAGACGATGACGAT 179

RESULT 10
US-10-092-750-153
; Sequence 153, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-750-153

Alignment Scores:
Pred. No.: 0.00173 Length: 1101
Score: 125.50 Matches: 55
Percent Similarity: 37.10% Conservativeness: 14
Best Local Similarity: 29.57% Mismatches: 67
Query Match: 11.78% Indels: 50
```

```
Pred. No.: 2.43e-10 Length: 105
Score: 178.00 Matches: 34
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.71% Indels: 0
DB: 15 Gaps: 0

US-09-508-832-10 (1-198) x US-10-092-750-153 (1-105)
Qy 132 AlaSerMetArgGlnAlaGluProAlaAspMetArgProGluIleTrpIleAlaGlnGlu 151
Db 1 GCTTCCATGAGCGAGGCTGAACCTGCAGATATGCGCCAGAGATATGATGCCCCAAGAG 60
Qy 152 LeuArgArgIleGlyAspGluPheAsnAlaTyTrTyAlaArg 165
Db 61 TTGCGGCGTATTGAGACGAGTTTAAACGCTTACTATGCAAGG 102

RESULT 11
US-10-282-122A-7256/c
; Sequence 7256, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7256
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-7256

Alignment Scores:
Pred. No.: 0.00173 Length: 1101
Score: 125.50 Matches: 55
Percent Similarity: 37.10% Conservativeness: 14
Best Local Similarity: 29.57% Mismatches: 67
Query Match: 11.78% Indels: 50
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Db 133617 CTGTGTCGCCAGCGATCAGTCGACTCGGCCAGGTGCGCGCTGAGGAGAAAGCTCCCGG 133558
Qy 27 nLeuArgProGlyAlaProThrSer-----LeuGln-ThrGluProGlnG 42
Db 133557 TCTCCGCCCGCGCGCCCTCGCTCCGACGCCCGCCACATCCGTTTCCGCGCCAGAGT 133498
Qy 42 lYAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerProGlnG 62
Db 133497 CTCAGCCAGCAGCTCAACCGCGCGCTCGCGCCCGCGCCGCCACCGCGCGCGCGGCC 133438
Qy 62 lYProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPheIleP 82
Db 133437 CGCTCCGAGCGCGCGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 133396
Qy 82 heMetArgSerSerLeuLeuSerArgSerSerSerGlyTyPheSerPheAspThrA 102
Db 133395 CTCGCCACGGGCTGCTGTGCTCTGCTCGGTCCCTCTCCGCCCGCTGCTGCTGCTGCT 133336
Qy 102 spArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProCysG 122
Db 133335 CTCTCCCTCTTCTCTCAGAGGATGTCGGGCTTCCAGATCAACCTCAACC-----C 133285
Qy 122 lnaAlaPheAsnHisTyRLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspM 142
Db 133284 GCTCAAGGAGCAGCTCGGCTTCATCAAGGCTCTCGAGTGGGTGAGTGCAGCGCGCGCG 133225
Qy 142 etArgProGluIleTrpIleAlaGlnGluLeuArgArgIleGlyAsp 157
Db 133224 CCAGCGCGCGCTCGCGCTCGCGCGCGCGCGCGCTTAGCGG---GGAGAC 133181
RESULT 14
US-10-981-277-22/c
; Sequence 22, Application US/10981277
; Publication No. US20050181389A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Compositions and Methods for Glioma Classification
; FILE REFERENCE: 03-968-US
; CURRENT APPLICATION NUMBER: US/10/981,277
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,817
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 151882
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-981-277-22
Alignment Scores:
Pred. No.: 1.99 Length: 151882
Score: 120.50 Matches: 46
Percent Similarity: 45.22% Conservative: 25
Best Local Similarity: 23.30% Mismatches: 69
Query Match: 11.31% Indels: 17
Gaps: 4
DB: 24
US-09-508-832-10 (1-198) x US-10-981-277-22 (1-151882)
Qy 8 ValSerSerGluCysAspArgGluGlyArg-GlnLeuGlnProAlaGluArgProGln 27
Db 89481 CTGTGTCGCCAGCGATCAGTCGACTCGGCCAGGTGCGGCTGAGGAGAGCTCCCGG 89422
Qy 27 nLeuArgProGlyAlaProThrSer-----LeuGln-ThrGluProGlnG 42
Db 89421 TCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 89362
Qy 42 lYAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerProGlnG 62
Db 89361 CTCAGCCAGCAGCTCAACCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 89302
```

```
Qy 62 lYProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPheIleP 82
Db 89301 GCGCTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 89260
Qy 82 heMetArgSerSerLeuLeuSerArgSerSerSerGlyTyPheSerPheAspThrA 102
Db 89259 CTCGCCACCGCGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 89200
Qy 102 spArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProCysG 122
Db 89199 CTCTCCCTCTTCTCTCAGAGGATGTCGGGCTTCCAGATCAACCTCAACC-----C 89149
Qy 122 lnaAlaPheAsnHisTyRLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspM 142
Db 89148 GCTCAAGGAGCAGCTCGGCTTCATCAAGGCTCTCGAGTGGGTGAGTGCAGCGCGCGCG 89089
Qy 142 etArgProGluIleTrpIleAlaGlnGluLeuArgArgIleGlyAsp 157
Db 89088 CCAGCGCGCGCTCGCGCTCGCGCGCGCGCGCGCTTAGCGG---GGAGAC 89045
RESULT 15
US-10-158-160A-14/c
; Sequence 14, Application US/10158160A
; Publication No. US20030059805A1
; GENERAL INFORMATION:
; APPLICANT: RAPPOLD-HOERBRAND, GUDRUN
; TITLE OF INVENTION: HUMAN GROWTH GENE AND SHORT STATURE GENE REGION
; FILE REFERENCE: 108351-00004
; CURRENT APPLICATION NUMBER: US/10/158,160A
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 09/147,699
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: PCT/EP97/05355
; PRIOR FILING DATE: 1997-09-29
; PRIOR APPLICATION NUMBER: 60/027,633
; PRIOR FILING DATE: 1996-10-01
; PRIOR APPLICATION NUMBER: EP/97100583.0
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-158-160A-14
Alignment Scores:
Pred. No.: 0.412 Length: 32367
Score: 119.50 Matches: 60
Percent Similarity: 41.24% Conservative: 13
Best Local Similarity: 33.90% Mismatches: 59
Query Match: 11.22% Indels: 45
Gaps: 11
DB: 15
US-09-508-832-10 (1-198) x US-10-158-160A-14 (1-32367)
Qy 9 SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgProPro 26
Db 14144 TCCCCAGCCTCTCTCCCGGACACACAGGTGTCAGAGCTCTCCCGGGTCCACAGTCCCA 14085
Qy 27 GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnGln 42
Db 14084 AGGCTCTCTCCGAGACACAGGTCTCCCGAGGACACAGGTCTCCCGAGGATCCCAAGG 14025
Qy 42 lYAsnProGlu-----GlyAsnHisGlyGlyGln 51
Db 14024 CTCTCCAGGACACACAGGTCTCCCGAGGACACAGGTCTCCCGAGGATCCCAAGCTCTCC 13965
Qy 51 uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaProProAlaSe 69
Db 13964 CGGGTCTACTAGGTCTCCCAAGGACATCCCGAGACACACAGGTCTCCCAAGGCTCTTCCA 13905
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QY 69 rProGlyProPheAla-----ThrArgSerProLeuPheIlePheMetArgAr 85
Db 13904 ACCAGGTCCCAAGGCTCTCCCAAGGACACCAAGGTCTCCCGGTACCCAG 13845
QY 85 gSerSerLeuLeuSerArg---SerSerSerGlyTyrPheSerPheAspThr----- 101
Db 13844 GTCCCAAGGCTCTCCCAAGGTCACCAAGGCTCTCTGGGACACCAAGGTGTC 13785
QY 102 -----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThrPro----- 117
Db 13784 AAGCCTCTCCCGGACACCAAGTCCCAAGCC-----TCTCCCGGACACCAAGGTC 13734
QY 118 -----SerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMetA 132
Db 13733 CCCAAGCCTCTCCCGGCTCACCAAGATCTCCCAAGCCTCTCCCAAGGACACCAAGGTCCCAAG 13674
QY 132 laSerMetArg-----GlnAlaGluProAlaAspMetArg 143
Db 13673 CCTCTCCCAAGGACACCAAGGTCCCAAGCCTCTCTCCCAAGGACACCAAGG 13627

Search completed: November 12, 2005, 08:27:46
Job time : 849 secs

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OM protein - protein search, using sw model

Run on: November 12, 2005, 04:59:33 ; Search time 28 Seconds
(without alignments)
527.876 Million cell updates/sec

Title: US-09-508-832-10

Perfect score: 1065

Sequence: 1 MAKQPSDVSSCDREGROLQ.....PRMVLRLRYIVRLVWRMH 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696	65.4	138	4	US-09-949-016-11305
2	144	13.5	27	4	US-09-544-664B-19
3	114	10.7	160	4	US-09-252-991A-27091
4	111.5	10.5	886	2	US-08-474-379C-65
5	111.5	10.5	886	3	US-09-146-249A-65
6	111.5	10.5	886	3	US-08-206-188B-65
7	111.5	10.5	901	4	US-09-917-254-93
8	108.5	10.2	885	2	US-08-577-492-33
9	108.5	10.2	885	3	US-09-079-630-33
10	103	9.7	1706	4	US-09-252-991A-31760
11	100	9.4	607	4	US-09-949-016-7817
12	100	9.4	627	4	US-08-487-596-6
13	100	9.4	627	4	US-08-660-451A-6
14	99	9.3	228	3	US-09-219-849-38
15	99	9.3	375	4	US-09-600-932-29
16	99	9.3	1057	3	US-08-931-820-4
17	99	9.3	1078	3	US-08-963-825-21
18	99	9.3	1078	3	US-09-500-811-21
19	99	9.3	1078	3	US-09-570-573-21
20	99	9.3	1078	3	US-09-548-608-21
21	98	9.2	349	4	US-09-252-991A-29455
22	97.5	9.2	1505	4	US-09-538-092-1102
23	97	9.1	372	4	US-09-252-991A-32717
24	95.5	9.0	50	4	US-09-621-976-5959
25	95	8.9	1516	4	US-09-949-016-8209
26	94.5	8.9	132	4	US-09-489-039A-9920
27	94.5	8.9	280	3	US-09-247-155-178

28	94.5	8.9	684	4	US-09-961-403-5	Sequence 5, Appli
29	94.5	8.9	1184	4	US-09-266-225D-18	Sequence 18, Appli
30	94.5	8.9	1185	3	US-09-041-886-23	Sequence 23, Appli
31	94.5	8.9	1185	4	US-09-538-092-1209	Sequence 1209, Ap
32	94	8.8	322	4	US-09-949-016-8332	Sequence 8332, Ap
33	94	8.8	562	4	US-09-879-752-12	Sequence 12, Appli
34	94	8.8	580	3	US-08-906-865-1	Sequence 1, Appli
35	94	8.8	580	4	US-09-129-668-1	Sequence 1, Appli
36	94	8.8	627	2	US-08-466-589-6	Sequence 6, Appli
37	94	8.8	627	2	US-08-700-636-6	Sequence 6, Appli
38	94	8.8	627	3	US-08-467-574-6	Sequence 6, Appli
39	94	8.8	627	3	US-09-217-345-6	Sequence 6, Appli
40	94	8.8	627	4	US-09-892-985-6	Sequence 6, Appli
41	93.5	8.8	245	4	US-09-311-021-104	Sequence 104, App
42	93.5	8.8	434	2	US-08-710-249-4	Sequence 4, Appli
43	93.5	8.8	434	3	US-09-220-157A-4	Sequence 4, Appli
44	93.5	8.8	902	1	US-08-396-479B-6	Sequence 6, Appli
45	93.5	8.8	902	1	US-08-818-823-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-11305
; Sequence 11305, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11305
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11305

Query Match 65.4%; Score 696; DB 4; Length 138;
Best Local Similarity 69.7%; Pred. No. 1.7e-63;
Matches 138; Conservative 0; Mismatches 0; Indels 60; Gaps 1;
QY 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSLQTEPQGNPEGNHGGEDSCPHGSP 60
DB 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSLQTEPQ----- 41
QY 61 QGFLAPPASPGFATRSPLIFMRSSLSRSSSGYFSFDTRSPAPMSCDKSTQTPSP 120
DB 42 -----DRSPAPMSCDKSTQTPSP 60
QY 121 COAFNHYLSAMASMRQAEPAEMRPEIWTAEQLRIGDEFNAYARRVFLNNYQAAEDHPR 180
DB 61 COAFNHYLSAMASMRQAEPAEMRPEIWTAEQLRIGDEFNAYARRVFLNNYQAAEDHPR 120
QY 181 MVILRLRYIVRLVWRMH 198
DB 121 MVILRLRYIVRLVWRMH 138
RESULT 2
US-09-544-664B-19
; Sequence 19, Application US/09544664B
; Patent No. 6713280

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/ GENERAL INFORMATION:
/ APPLICANT: Huang, Ziwei
/ APPLICANT: Wang, Jialun
/ APPLICANT: Zhang, Zhijia
/ APPLICANT: Shan, Simei
/ APPLICANT: Lu, Zhixian
/ TITLE OF INVENTION: Enhancement of Peptide Cellular Uptake
/ FILE REFERENCE: 8321-66
/ CURRENT APPLICATION NUMBER: US/09/544,664B
/ CURRENT FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: PCT/US00/09352
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/128,202
/ PRIOR FILING DATE: 1999-04-07
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 19
/ LENGTH: 27
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide
/ OTHER INFORMATION: segment from BH3 domain of a Bcl-2 superfamily
/ OTHER INFORMATION: polypeptide
US-09-544-664B-19

Query Match      13.5%; Score 144; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 DMRPEIWIQAQLRRIGDGFNAYARRV 167
DB 1 DMRPEIWIQAQLRRIGDGFNAYARRV 27

RESULT 3
US-09-252-991A-27091
/ Sequence 27091, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 27091
/ LENGTH: 160
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27091

Query Match      10.7%; Score 114; DB 4; Length 160;
Best Local Similarity 30.6%; Pred. No. 0.00065;
Matches 44; Conservative 10; Mismatches 56; Indels 34; Gaps 7;

QY 21 PAERPPQLRPG---APTSLQTEPQ-----NPEGNH-----GGEDSCPHGSPQGPLAPPAS 69
DB 18 PRKKPPARPQPCAPGRLPSPRPGGAAGNAPPGRGSSATPGSGGAPPAPPAR 77
QY 70 PGPFATRSPLFIPIRRSSLLSRSSSGYFSDTD-RSPAPMS-----CDKSTQTPSP 119
DB 78 RARRAGRDD-----GRSAATAR-----DRDSRSPAPRGAGRARASGCRPAGRPPR 124
QY 120 PCQAFNHYLSAMASMRQAEPADMR 143
DB 125 PASASADRLARVATRHAGRPVGVR 148
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RESULT 4
US-08-474-379C-65
/ Sequence 65, Application US/08474379C
/ Patent No. 5977305
/ GENERAL INFORMATION:
/ APPLICANT: Wigler, Michael H.
/ APPLICANT: Colicelli, John J.
/ TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
/ TITLE OF INVENTION: PROCESSES
/ NUMBER OF SEQUENCES: 88
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive/6300 Sears Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States of America
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/474,379C
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/511,715
/ FILING DATE: 20-APR-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/206,188
/ FILING DATE: 01-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/688,352
/ FILING DATE: 19-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clough, David W.
/ REGISTRATION NUMBER: 36,107
/ REFERENCE/DOCKET NUMBER: 27866/32771
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ INFORMATION FOR SEQ ID NO: 65:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 886 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-474-379C-65

Query Match      10.5%; Score 111.5; DB 2; Length 886;
Best Local Similarity 27.5%; Pred. No. 0.011;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;

QY 6 SDVSSCEDRGRLQLOPARPPQL-----RPGATSLQTEPQ-----GNPGRNHGG----- 50
DB 49 SDSAERAERERQPHRIERADAMDTSRPLRTTMSWPSFHGTGTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-QGPLAPPASPGPFATRSPLFIPIRRSSLLSRSSSGYFSDTDSPAPMS 109
DB 109 EAENGTPSPGRSPLDSQASPG-LVLHAGAATSQRRESFLYRSDSDY-----DMSPKTWS 162
QY 110 CDKSTQTPSPPCQAFNHYLSAMASMRQAEPADMRPEIWIQAQLRRIGDGFN 160
DB 163 RN-----SSVTSEAHAEADLIVTPPAQVLASLRVRSNFS 196

RESULT 5
US-09-146-249A-65
/ Sequence 65, Application US/09146249A
/ Patent No. 6069240
/ GENERAL INFORMATION:
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APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE: 20-APR-1990
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 886 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-146-249A-65

Query Match 10.5%; Score 111.5; DB 3; Length 886;
Best Local Similarity 27.5%; Pred. No. 0.011; Mismatches 18; Indels 39; Gaps 7;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQQAERPPQL-----RPGAPTSIQTEPQ-----GNPEGNHGG----- 50
DB 49 SDSAERAERQPHRPIERADAMDTSDRPLGRTTMSWPSSFHGTGTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-QGPLAPPSPGPFATRSPLFIFMRSSLLRSSSGYFSFTDRSPAPMS 109
DB 109 EAENGTPSPGRSPLDSQSPG-LVLHAGAATSQRRSFYRSDSDY-----DMSPKTMS 162
QY 110 CDKSTQTSPPCQAFNHYLSAMSRQAEPMRPEIWAQELRRIGDEFN 160
DB 163 RN-----SSVTSEAHEDLIVTPFAQVLASLRVRSNFS 196

RESULT 6
US-08-206-188B-65
Sequence 65, Application US/08206188B
Patent No. 6100025
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 886 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-206-188B-65

Query Match 10.5%; Score 111.5; DB 3; Length 886;
Best Local Similarity 27.5%; Pred. No. 0.011; Mismatches 18; Indels 39; Gaps 7;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQQAERPPQL-----RPGAPTSIQTEPQ-----GNPEGNHGG----- 50
DB 49 SDSAERAERQPHRPIERADAMDTSDRPLGRTTMSWPSSFHGTGTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-QGPLAPPSPGPFATRSPLFIFMRSSLLRSSSGYFSFTDRSPAPMS 109
DB 109 EAENGTPSPGRSPLDSQSPG-LVLHAGAATSQRRSFYRSDSDY-----DMSPKTMS 162
QY 110 CDKSTQTSPPCQAFNHYLSAMSRQAEPMRPEIWAQELRRIGDEFN 160
DB 163 RN-----SSVTSEAHEDLIVTPFAQVLASLRVRSNFS 196

RESULT 7
US-09-917-254-93
Sequence 93, Application US/09917254
Patent No. 6703204
GENERAL INFORMATION:
APPLICANT: Mutter, George
APPLICANT: Baak, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/7224(JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 93
LENGTH: 901
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-917-254-93

Query Match 10.5%; Score 111.5; DB 4; Length 901;
Best Local Similarity 27.5%; Pred. No. 0.011; Mismatches 18; Indels 39; Gaps 7;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQQAERPPQL-----RPGAPTSIQTEPQ-----GNPEGNHGG----- 50
DB 64 SDSAERAERQPHRPIERADAMDTSDRPLGRTTMSWPSSFHGTGTGSGGAGGSSRRF 123


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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31760
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31760

Query Match          9.4%; Score 103; DB 4; Length 1706;
Best Local Similarity 29.7%; Pred. No. 0.19;
Matches 52; Conservative 17; Mismatches 56; Indels 50; Gaps 13;

QY  2 AKQPSDVSECDREGRLQPAERPP-QLRPGAPTSLOTPEQGNPGNHGGEGDS---CPH 57
DB  435 ARPPAALPARA-RRGRRRQPPGRPRRLRPGAPVAAAPATGG-AATEFGAGDSRRHCRS 492
QY  58 GS-----PQGLA-----PPASPGPFATR-----SPLFIMRRSSLLSRSSSGYFSDT 101
DB  493 GTDRCPRPQPAARDPGSGWPGSAARRAARGDP-----HRRETAL-RSAA----- 540
QY  102 DRSPAPMSCDKSTQTFSPPCQAFNHYLSAMASMQA-----EPADMRP 144
DB  541 -RRPR-RRADPPGRTPAQPGQ--TEGARRLARRRTAGTAAPHRHQPPQAPGPRP 591

RESULT 11
US-09-949-016-7817
; Sequence 7817, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7817
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7817

Query Match          9.4%; Score 100; DB 4; Length 607;
Best Local Similarity 26.4%; Pred. No. 0.099;
Matches 33; Conservative 15; Mismatches 43; Indels 34; Gaps 5;

QY  1 MAKQPSDVSECDREGRLQPAERPPQLRPGAPTSLOTPEQGNPGNHGGEGDSCTPHGSP 60
DB  337 LMKRPSVVKDNCRRLLIESMHKMASAPRWP-----EPEGEPPATSGTQSLHPPSPSF 388
QY  61 QGPLAPPASPGPFATRSPFLFIMRRSSLLSRSSSGYFSDTDTRSP--APMSCDKSTQTPS 118
DB  389 CVPILDVPAEPGP-SCKSP-----SDQLPPQPPLEAKASPHPS 425
QY  119 P-PCQ 122
DB  426 PGPCR 430

RESULT 12
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US-08-487-596-6
; Sequence 6, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-487-596-6

Query Match          9.4%; Score 100; DB 4; Length 627;
Best Local Similarity 26.4%; Pred. No. 0.1;
Matches 33; Conservative 15; Mismatches 43; Indels 34; Gaps 5;

QY  1 MAKQPSDVSECDREGRLQPAERPPQLRPGAPTSLOTPEQGNPGNHGGEGDSCTPHGSP 60
DB  357 LMKRPSVVKDNCRRLLIESMHKMASAPRWP-----EPEGEPPATSGTQSLHPPSPSF 408
QY  61 QGPLAPPASPGPFATRSPFLFIMRRSSLLSRSSSGYFSDTDTRSP--APMSCDKSTQTPS 118
DB  409 CVPILDVPAEPGP-SCKSP-----SDQLPPQPPLEAKASPHPS 445
QY  119 P-PCQ 122
DB  446 PGPCR 450
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OM protein - protein search, using sw model

Run on: November 12, 2005, 06:25:58 ; Search time 80 Seconds
(without alignments)
1035.563 Million cell updates/sec

Title: US-09-508-832-10
Perfect score: 1065
Sequence: 1 MAKQPSVSSCDREGROLQ.....PRMVLRLRYIVRLVWRMH 198

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Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696	65.4	138	14	US-10-092-750-241
2	696	65.4	138	16	US-10-755-889-16
3	497	46.7	92	18	US-10-450-783-31522
4	194	18.2	64	9	US-09-971-980-62
5	194	18.2	64	18	US-10-966-576-62
6	178	16.7	35	14	US-10-092-750-1
7	164	15.4	50	9	US-09-971-980-64
8	164	15.4	50	18	US-10-966-576-64
9	114	10.7	949	16	US-10-437-963-192001
10	111.5	10.5	410	16	US-10-437-963-196665
11	111.5	10.5	886	15	US-10-332-065-2

12	111.5	10.5	886	16	US-10-408-765A-261	Sequence 261, App
13	111.5	10.5	901	18	US-10-450-763-37429	Sequence 37429, A
14	111.5	10.5	1029	14	US-10-257-909A-24	Sequence 24, Appl
15	111.5	10.5	1124	14	US-10-257-909A-6	Sequence 6, Appl
16	111.5	10.5	1132	14	US-10-257-909A-4	Sequence 4, Appl
17	111.5	10.5	1132	14	US-10-257-909A-8	Sequence 8, Appl
18	111.5	10.5	1132	14	US-10-257-909A-32	Sequence 32, Appl
19	111.5	10.4	531	18	US-10-450-763-51899	Sequence 51899, A
20	110	10.3	1764	16	US-10-437-963-192101	Sequence 192101,
21	109	10.2	1680	16	US-10-437-963-192175	Sequence 192175,
22	108	10.1	1851	16	US-10-437-963-192171	Sequence 192171,
23	107	10.0	1694	16	US-10-437-963-192057	Sequence 192057,
24	106.5	10.0	783	14	US-10-241-220-93	Sequence 93, Appl
25	106.5	10.0	783	14	US-10-301-822-59	Sequence 59, Appl
26	106.5	10.0	783	15	US-10-295-027-1191	Sequence 1191, Ap
27	106.5	10.0	783	16	US-10-872-972-93	Sequence 93, Appl
28	106.5	10.0	783	16	US-10-872-991-93	Sequence 93, Appl
29	106.5	10.0	783	17	US-10-916-064-6	Sequence 6, Appl
30	106.5	10.0	783	18	US-10-756-149-5686	Sequence 5686, Ap
31	106.5	10.0	783	18	US-10-983-340-10	Sequence 10, Appl
32	106.5	10.0	950	20	US-11-097-143-41331	Sequence 41331, A
33	106	10.0	20	16	US-10-658-028A-2	Sequence 2, Appl
34	106	10.0	810	14	US-10-156-761-10081	Sequence 10081, A
35	106	10.0	1347	16	US-10-437-963-191996	Sequence 191996,
36	106	10.0	1416	16	US-10-437-963-192143	Sequence 192143,
37	106	10.0	1487	16	US-10-437-963-188109	Sequence 188109,
38	106	10.0	1848	16	US-10-437-963-192129	Sequence 192129,
39	105.5	9.9	574	14	US-10-168-097A-76	Sequence 76, Appl
40	105.5	9.9	574	14	US-10-239-431A-38	Sequence 38, Appl
41	104.5	9.8	706	15	US-10-424-599-218604	Sequence 218604,
42	104	9.8	1504	15	US-10-374-780A-1457	Sequence 1457, Ap
43	104	9.8	1504	16	US-10-437-963-192134	Sequence 192134,
44	104	9.8	1851	16	US-10-437-963-192177	Sequence 192177,
45	103.5	9.7	248	16	US-10-425-115-208167	Sequence 208167,

ALIGNMENTS

RESULT 1
US-10-092-750-241
; Sequence 241, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-241

Query Match 65.4%; Score 696; DB 14; Length 138;
Best Local Similarity 69.7%; Pred. No. 1.2e-50;
Matches 138; Conservative 0; Mismatches 0; Indels 60; Gaps 1;
QY 1 MAKQPSVSSCDREGROLQPAERPPQLRPGAPTSLSQTEPQGNPGNHGEGSDSCPHGSP 60
DB 1 MAKQPSVSSCDREGROLQPAERPPQLRPGAPTSLSQTEPQGNPGNHGEGSDSCPHGSP 41
QY 61 QGLAPPASPGPFATRSPLFIEMRSSLLSRSSGVFSFDTDRSPAPMSCDKSTOTPSPP 120
DB 42 -----DRSPAPMSCDKSTOTPSPP 60

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QY 121 COAFNHYLSAMSMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPR 180
DB 61 COAFNHYLSAMSMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPR 120

QY 181 MVILRLRYIVRLVWRMH 198
DB 121 MVILRLRYIVRLVWRMH 138

RESULT 2
US-10-755-889-16
; Sequence 16, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-16

Query Match 65.4%; Score 696; DB 16; Length 138;
Best Local Similarity 69.7%; Pred. No. 1.2e-50;
Matches 138; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

QY 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSIQTEPQGNPEGNHGEGDSCPHGSP 60
DB 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSIQTEPQ----- 41

QY 61 QGPLAPPASPGPFATRSPLFIEMRSSLSRSSGYSFDTDRSPAPMSCDKSTQTPSP 120
DB 42 -----DRSPAPMSCDKSTQTPSP 60

QY 121 COAFNHYLSAMSMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPR 180
DB 61 COAFNHYLSAMSMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPR 120

QY 181 MVILRLRYIVRLVWRMH 198
DB 121 MVILRLRYIVRLVWRMH 138

RESULT 3
US-10-450-763-31522
; Sequence 31522, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 31522
; LENGTH: 92
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-31522

Query Match 46.7%; Score 497; DB 18; Length 92;
Best Local Similarity 100.0%; Pred. No. 4e-34;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSIQTEPQGNPEGNHGEGDSCPHGSP 60

QY 61 QGPLAPPASPGPFATRSPLFIEMRSSLSRS 92
DB 61 QGPLAPPASPGPFATRSPLFIEMRSSLSRS 92

RESULT 4
US-09-971-980-62
; Sequence 62, Application US/09971980
; Patent No. US20020164349A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruses
; TITLE OF INVENTION: Pestiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020164349A1el Sequence
US-09-971-980-62

Query Match 18.2%; Score 194; DB 9; Length 64;
Best Local Similarity 68.8%; Pred. No. 7.2e-09;
Matches 44; Conservative 8; Mismatches 8; Indels 4; Gaps 3;

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DB 3 ASIRQSQEPEDLRPEIRI-QELRRIGDEFNETYTRRVFA-DYREAEDHPQWVILQLLRF 60

QY 190 IVRL 193
DB 61 IPRL 64

RESULT 5
US-10-966-576-62
; Sequence 62, Application US/10966576
; Publication No. US20050226849A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruses
; TITLE OF INVENTION: Pestiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/10/966,576
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US/09/971,980
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
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RESULT 7
US-09-971-380-64
; Sequence 64, Application US/09971980
; Patent No. US20020164349A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Meth
; TITLE OF INVENTION: Festiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 50
; TYPE: EXT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020164349A1el

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RESULT 9
US-10-437-963-192001
; Sequence 192001, Application US/10437963
; Publication No. US20040123343A1
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; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbasuk, Brad
; APPLICANT: Li, Ping
;
; TITLE OF INVENTION: Rice Nucleic Acid M
;
; TITLE OF INVENTION: Plants and Uses Th
;
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,9
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
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; SEQ ID NO 192001
; LENGTH: 949
; TYPE: PRT
; ORGANISM: Oryza sativa
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; FEATURE:
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; OTHER INFORMATION: Clone ID: PAT_MRT45
US-10-437-963-192001

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QY 64 LAPPA-----SPGFATRSPLFIEMRSSLLSSSGYFSFDTDRSPAPMSCK--STQTP 117
DB 259 SAVQFCRCNQMGHYARQCP-----QNPITNSCHANGSTARTPTFAAAQSRPSTQAS 310
QY 118 SPPCAFNHYLSAMASMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEED 177
DB 311 GGGSRASHFRGRVNHVHQAETAQAPDVVMGARVFSKIDLRSGYHQLKI-----RSED 364
QY 178 HPR 180
DB 365 IPK 367

RESULT 10
US-10-437-963-196665
; Sequence 196665, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 196665
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(410)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92495C.1.pap
US-10-437-963-196665

Query Match 10.5%; Score 111.5; DB 16; Length 410;
Best Local Similarity 28.5%; Pred. No. 0.5;
Matches 49; Conservative 10; Mismatches 50; Indels 63; Gaps 9;
QY 17 RQLQPAER-PPQLRPGAPTSLSQTEPQCNPEGNHGEG-----DSCPHGSPQGP 64
DB 142 RQSGPARRGPPAHROQAPTRRSRSPSPHP-THPPRGAPCSFGEDSCTWPSCTPLPRHQ 200
QY 65 -----APPASGPFATRSPLFIEMRSS-----PXLHLVLTSPAKKPTNPSPRISPTSPR 255
DB 201 RRRHGCAPAPSAATAASPAPETP-----PXLHLVLTSPAKKPTNPSPRISPTSPR 255
QY 88 LLRSRSSGYFSFDTDRSPAPMSCKSTQTPSPCAFNHYLSAMASMRQAE 139
DB 256 PLHSSTPG-----AADSPAPAS--RSPSPSPLEALPSRLT--VSITPARP 299

RESULT 11
US-10-332-065-2
; Sequence 2, Application US/10332065
; Publication No. US20040018504A1

; GENERAL INFORMATION:
; APPLICANT: BJORN, Sara Petersen et al.
; TITLE OF INVENTION: A METHOD FOR EXTRACTING QUANTITATIVE
; TITLE OF INVENTION: INFORMATION RELATING TO INTERACTIONS BETWEEN CELLULAR
; FILE REFERENCE: 3759-0129P
; CURRENT APPLICATION NUMBER: US/10/332,065
; CURRENT FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 886
; TYPE: PRT
; ORGANISM: Aequoria victoria and Homo sapiens
US-10-332-065-2

Query Match 10.5%; Score 111.5; DB 15; Length 886;
Best Local Similarity 27.5%; Pred. No. 1.2;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQPAERPPQL-----RPGAPTSLSQTEPQ-----GNPEGNHG----- 50
DB 49 SDSAERAERERQPHRIERADAMDTSDRPLGRLTTRMSWPSFPHGTGTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-OGPLAPPASPGPPATRSPLFIEMRSSLLSSSGYFSFDTDRSPAPMS 109
DB 109 EAENGFTSPGSRPLDSQASPG-LVLHGAATSQRRSEFLYRSDSY-----DMSFKTMS 162
QY 110 CDKSTQTPSPPCQAFNHYLSAMASMRQAEADMRPEIWIQAELRRIGDEFN 160
DB 163 RN-----SSVTSEAHAEADLIVTPFAQVLASLRVRSNFS 196

RESULT 12
US-10-408-765A-261
; Sequence 261, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 886
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-261

Query Match 10.5%; Score 111.5; DB 16; Length 886;
Best Local Similarity 27.5%; Pred. No. 1.2;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQPAERPPQL-----RPGAPTSLSQTEPQ-----GNPEGNHG----- 50
DB 49 SDSAERAERERQPHRIERADAMDTSDRPLGRLTTRMSWPSFPHGTGTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-OGPLAPPASPGPPATRSPLFIEMRSSLLSSSGYFSFDTDRSPAPMS 109
DB 109 EAENGFTSPGSRPLDSQASPG-LVLHGAATSQRRSEFLYRSDSY-----DMSFKTMS 162
QY 110 CDKSTQTPSPPCQAFNHYLSAMASMRQAEADMRPEIWIQAELRRIGDEFN 160
DB 163 RN-----SSVTSEAHAEADLIVTPFAQVLASLRVRSNFS 196

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Maximum Match 100%

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- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	394.4	66.2	44479	4	US-09-949-016-17176 Sequence 17176, A
2	294	49.3	417	4	US-09-949-016-5434 Sequence 5434, Ap
3	176	29.5	398	4	US-09-621-976-2153 Sequence 2153, Ap
4	113	19.0	477	4	US-09-621-976-2099 Sequence 2099, Ap
5	110	18.5	601	4	US-09-949-016-18929 Sequence 18929, Ap
6	37	6.2	2110	4	US-09-949-016-1105 Sequence 1105, Ap
7	37	6.2	2111	4	US-09-949-016-1173 Sequence 1173, Ap
8	37	6.2	4047	4	US-09-081-385-1 Sequence 1, Appl
9	37	6.2	4047	4	US-09-081-385-177 Sequence 147, App
10	37	6.2	40546	4	US-09-949-016-12847 Sequence 12847, A
11	37	6.2	40546	4	US-09-949-016-12915 Sequence 12915, A
12	36.2	6.1	12787	4	US-09-949-016-16359 Sequence 16359, A
13	36.2	6.1	15141	4	US-09-949-016-14869 Sequence 14869, A
14	36.2	6.1	17740	4	US-09-949-016-13086 Sequence 13086, A
15	36	6.0	7218	1	US-08-232-463-14 Sequence 14, Appl
16	35.2	5.9	1776	4	US-09-252-991A-10145 Sequence 10145, A
17	35.2	5.9	2097	4	US-09-252-991A-9932 Sequence 9932, Ap
18	35.2	5.9	2163	4	US-09-252-991A-10079 Sequence 10079, A
19	35.2	5.9	146039	4	US-09-949-016-12449 Sequence 12449, A
20	35	5.9	678	4	US-09-902-540-9456 Sequence 9456, Ap
21	35	5.9	15095	4	US-09-902-540-1077 Sequence 1077, Ap
22	34.4	5.8	42610	4	US-09-949-016-13882 Sequence 13882, A
23	33.8	5.7	11002	4	US-09-949-016-17471 Sequence 17471, A
24	33.8	5.7	11002	4	US-09-949-016-17472 Sequence 17472, A
25	33.8	5.7	11002	4	US-09-949-016-17473 Sequence 17473, A
26	33.4	5.6	1167	4	US-09-252-991A-14177 Sequence 14177, A
27	33.2	5.6	3758	4	US-09-799-451-454 Sequence 454, App

C	28	33	5.5	505	4	US-09-621-976-15639	Sequence 15639, A
	29	33	5.5	1464	1	US-08-243-542-5	Sequence 5, Appl
	30	33	5.5	1464	1	US-08-477-407-5	Sequence 5, Appl
	31	33	5.5	1464	1	US-08-484-355-5	Sequence 5, Appl
	32	33	5.5	2913	1	US-08-243-542-7	Sequence 7, Appl
	33	33	5.5	2913	1	US-08-477-407-7	Sequence 7, Appl
	34	33	5.5	2913	1	US-08-484-355-7	Sequence 7, Appl
	35	33	5.5	2923	1	US-08-243-542-6	Sequence 6, Appl
	36	33	5.5	2923	1	US-08-477-407-6	Sequence 6, Appl
	37	33	5.5	2923	1	US-08-484-355-6	Sequence 6, Appl
	38	33	5.5	3167	4	US-09-949-016-3734	Sequence 3734, Ap
	39	33	5.5	3167	4	US-09-949-016-3735	Sequence 3735, Ap
	40	33	5.5	3183	1	US-08-243-542-8	Sequence 8, Appl
	41	33	5.5	3183	1	US-08-477-407-8	Sequence 8, Appl
	42	33	5.5	3183	1	US-08-484-355-8	Sequence 8, Appl
	43	32.8	5.5	31713	4	US-09-949-016-16960	Sequence 16960, A
	44	32.8	5.5	37155	4	US-09-949-016-16945	Sequence 16945, A
C	45	32.6	5.5	1128	4	US-09-252-991A-3879	Sequence 3879, Ap

ALIGNMENTS

RESULT 1
US-09-949-016-17176
; Sequence 17176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17176
; LENGTH: 44479
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(44479)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17176

Query Match	66.2%	Score	394.4;	DB	4;	Length	44479;
Best Local Similarity	99.7%	Pred. NO.	9.1e-120;				
Matches	395;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
QY	1	ATGCCAAAGCAACCTTCTGATGTAGTCTCAGTGTGACCGGAGAGGTAGACAATTGCAG	60				
Db	2001	ATGCCAAAGCAACCTTCTGATGTAGTCTGATGTGACCGGAGAGGTAGACAATTGCAG	2060				
QY	61	CCTCGGAGAGGCTCCCGAGCTCAGACTGGGGCCCTTACTCTCCTACAGACAGAGCCA	120				
Db	2061	CCTCGGAGAGGCTCCCGAGCTCAGACTGGGGCCCTTACTCTCCTACAGACAGAGCCA	2120				
QY	121	CAAGTAATCTTGAAGCAATCAGGAGTGAAGGGACAGTCCCGCCAGCCCTTTC	180				
Db	2121	CAAGTAATCTTGAAGCAATCAGGAGTGAAGGGACAGTCCCGCCAGCCCTTTC	2180				
QY	181	CAGGCCCGCTGGGCCCGCCAGCTTGGCCCTTTTGTCTTACAGATCCCGCTTTC	240				
Db	2181	CAGGCCCGCTGGGCCCGCCAGCTTGGCCCTTTTGTCTTACAGATCCCGCTTTC	2240				
QY	241	ATCTTTATGAGAAGATCTCCCTGCTGCTCGATCCTCGAGTGGGTATTTCTCTTTTGAC	300				

```
Db 2241 ATCTTTATGAGAAGATCTCCCTGCTGCTCATCTCCAGTGGGTATTTCTTTTGAC 2300
QY 301 ACAGACAGAGAGCCAGCAGCCCATGAGTTGTGACAAATCAACAAACCCCAAGTCTCTCT 360
Db 2301 ACAGACAGAGAGCCAGCAGCCCATGAGTTGTGACAAATCAACAAACCCCAAGTCTCTCT 2360
QY 361 TCCAGAGGCTTCAACCACTATCTCAGTGCATGGCT 396
Db 2361 TCCAGAGGCTTCAACCACTATCTCAGTGCATGGCT 2396

RESULT 2
US-09-949-016-5434
; Sequence 5434, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5434
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5434
```

```
Query Match 49.3%; Score 294; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.7e-87;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AGACAGGAGCCAGCAGCCCATGAGTTGTGACAAATCAACAAACCCCAAGTCTCTCTTG 362
Db 123 AGACAGGAGCCAGCAGCCCATGAGTTGTGACAAATCAACAAACCCCAAGTCTCTCTTG 182
QY 363 CCAGGCTTCAACCACTATCTCAGTGCATGGCTTCCATGAGGAGGCTGAACCTGCAGA 422
Db 183 CCAGGCTTCAACCACTATCTCAGTGCATGGCTTCCATGAGGAGGCTGAACCTGCAGA 242
QY 423 TATGCGCCAGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
Db 243 TATGCGCCAGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 302
QY 483 TTACTATGCAAGAGGGTATTTTGAATATTTACCAAGCAGCGGAGACCCACCGAAT 542
Db 303 TTACTATGCAAGAGGGTATTTTGAATATTTACCAAGCAGCGGAGACCCACCGAAT 362
QY 543 GGTATCTTACAGCTGTTACGTTACATTTCCGCTCGGTGTGGAGATGCATTG 596
Db 363 GGTATCTTACAGCTGTTACGTTACATTTCCGCTCGGTGTGGAGATGCATTG 416

RESULT 3
US-09-621-976-2153
; Sequence 2153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
```

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; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2153
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 18..239
; NAME/KEY: misc_feature
; LOCATION: 14
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-2153

Query Match 29.5%; Score 176; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 3.3e-48;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAAGGTAGACAAATTGCAG 60
Db 223 ATGGCAAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAAGGTAGACAAATTGCAG 282
QY 61 CTGCGGAGAGGCGCTCCCGAGCTCAGACCTGGGGGCCCTACCTCCCTACAGACAGAGCCA 120
Db 283 CTGCGGAGAGGCGCTCCCGAGCTCAGACCTGGGGGCCCTACCTCCCTACAGACAGAGCCA 342
QY 121 CAAGGTAATCTGAAGGCAATCACCGAGGTGAAGGGGACAGCTGCCCGACGGCAG 176
Db 343 CAAGGTAATCTGAAGGCAATCACCGAGGTGAAGGGGACAGCTGCCCGACGGCAG 398

RESULT 4
US-09-621-976-2099
; Sequence 2099, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2099
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 223..372
US-09-621-976-2099

Query Match 19.0%; Score 113; DB 4; Length 477;
Best Local Similarity 99.2%; Pred. No. 3.5e-27;
Matches 124; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGGCAAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAAGGTAGACAA-TTGC 59
Db 223 ATGGCAAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAAGGTAGACAA-TTGC 282
QY 60 GCCTGCGGAGAGGCGCTCCCGAGCTCAGACCTGGGGGCCCTACCTCCCTACAGACAGAGCC 119
Db 283 GCCTGCGGAGAGGCGCTCCCGAGCTCAGACCTGGGGGCCCTACCTCCCTACAGACAGAGCC 342
QY 120 ACAAG 124
Db 343 ACAAG 347

RESULT 5
```


US-09-949-016-189929
; Sequence 189929, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189929
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189929

Query Match 18.5%; Score 110; DB 4; Length 601;
Best Local Similarity 90.6%; Pred. No. 4e-26;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCATGAGCAGCTGAACCTCAGATATGCGCCAGAGATATGATGCCCCAAGAG 453
DB |||||
QY 230 GCTTCATGAGCAGCTGAACCTCAGATATGCGCCAGAGATATGATGCCCCAAGAG 289
DB |||||
QY 454 TTGCGCGGTATCGGAGACAGTTTAACTTACTATGCAAGGAGGTATTTTGAATAAT 513
DB |||||
QY 290 TTGCGCGGTATGAGAGAGTTTAACTTACTATGCAAGGAGGTATGATGTTTCT 349
DB |||||
QY 514 TACCAAGC 521
DB |||||
QY 350 TTACCCGC 357
DB |||||

RESULT 6

US-09-949-016-1105/c
; Sequence 1105, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 2110
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1105

Query Match 6.2%; Score 37; DB 4; Length 2110;
Best Local Similarity 53.9%; Pred. No. 0.17;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 64 GCGGAGAGCCCTCCCGAGCTGAGACCTGGGGCCCTTACCTCCCTACAGACAGCCACNA 123
DB |||||
QY 715 GCGTTGAATGTCCACAGCTCCACCTTGGCAGCCAGCGTCCCGCAGCAGCCTCAGGCGCG 656
DB |||||

QY 124 GGTAAATCCTGAAGCAATCAGGAGGTGAAGGGGACAGCTGCCCCCAGGAGCCCTCAG 183
DB |||||
QY 655 CGTCCACTTGTGCGGGGCTCGGGGTCGCGGGGACAGCTGCGGGCTCGGGCTCGGGCGA 596
DB |||||
QY 184 GCGCGCTGGCCCCACCTGCC 204
DB |||||
QY 595 GCGCGCGCGTGCACATGTC 575
DB |||||

RESULT 7

US-09-949-016-1173/c
; Sequence 1173, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1173
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1173

Query Match 6.2%; Score 37; DB 4; Length 2111;
Best Local Similarity 53.9%; Pred. No. 0.17;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 64 GCGGAGAGCCCTCCCGAGCTGAGACCTGGGGCCCTTACCTCCCTACAGACAGCCACAA 123
DB |||||
QY 715 GCGTTGAATGTCCACAGCTCCACCTTGGCAGCCAGCTCCCGCAGCAGCCTCAGGCGCG 656
DB |||||
QY 124 GGTAAATCCTGAAGCAATCAGGAGGTGAAGGGGACAGCTGCCCCCAGGAGCCCTCAG 183
DB |||||
QY 655 CGTCCACTTGTGCGGGGCTCGGGGTCGCGGGGACAGCTGCGGGCTCGGGCTCGGGCGA 596
DB |||||
QY 184 GCGCGCTGGCCCCACCTGCC 204
DB |||||
QY 595 GCGCGCGCGTGCACATGTC 575
DB |||||

RESULT 8

US-09-081-385-1/c
; Sequence 1, Application US/09081385
; Patent No. 6593456

GENERAL INFORMATION:

; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

```

, , OPERATING SYSTEM: Windows
, , SOFTWARE: FastSeq for Windows Version 2.0b
, , CURRENT APPLICATION DATA:
, , APPLICATION NUMBER: US/09/081.385
, , FILING DATE:
, , CLASSIFICATION:
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: 08/964,747
, , FILING DATE: 05-NOV-1997
, , APPLICATION NUMBER: 60/030,761
, , FILING DATE: 06-NOV-1996
, , ATTORNEY/AGENT INFORMATION:
, , NAME: Wu, Frank
, , REGISTRATION NUMBER: 41,386
, , REFERENCE/DOCKET NUMBER: 22000-20577.21
, , TELECOMMUNICATION INFORMATION:
, , TELEPHONE: 650-813-5600
, , TELEFAX: 650-494-0792
, , TELEX: 706141
, , INFORMATION FOR SEQ ID NO: 1:
, , SEQUENCE CHARACTERISTICS:
, , LENGTH: 4047 base pairs
, , TYPE: nucleic acid
, , STRANDEDNESS: double
, , TOPOLOGY: linear
, , MOLECULE TYPE: Genomic DNA
, , US-09-081-385-1

Query Match 6.2%; Score 37; DB 4;
Best Local Similarity 52.2%; Pred. No. 0.25;
Matches 82; Conservative 0; Mismatches

Qy 65 CGGAGAGGCCTCCCGAGCTCAGACCTGGGGGGCCCTTA
Db 203 CGAGGCGCGCCCGCGCGGCCCGCCACGCGCGCGCCCAT
Qy 125 GTAATCCTGAAGGCAATCACGGAGGCTGAAGGGGACAC
Db 143 GAGCTGGCGGCCCGCCCGAGCTGGAGAGCGCGGCCCGCA
Qy 185 GCCCGCTGGGCCCGCCAGCTGCCAGCCCTGGCCCTTTTGG
Db 83 CCACTCTGGCCCCCGAGCCCCCGCTGCTCGGAGTG

```

RESULT 9
US-09-081-385-147
Sequence 147, Application US/09081385
Patent No. 6591456
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,385
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 378...1795
; OTHER INFORMATION:
;
; US-09-081-385-147

Query Match          6.2%; Score 37; DB 4; Length 4047;
Best Local Similarity 52.2%; Pred. No. 0.25;
Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy      65  CGGAGAGGCGCTCCCGAGCTCAGAGCTGGGGCCCTACTCTCCTACAGACAGAGCCACAAG 124
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3845 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3904
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy      125  GTAATCTCTGAAGGCAATCAGCGAGGTGAAGGGGACAGCTGCCCGCCACCGGACCGCTCAGG 184
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3905 GAGCTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4001
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy      185  GCCCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 221
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3965 CCACTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4001
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 10
US-09-949-016-12847/c
; Sequence 12847, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12847
; LENGTH: 40546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12847

Query Match          6.2%; Score 37; DB 4; Length 40546;
Best Local Similarity 53.9%; Pred. No. 0.93;
Matches 76; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

          64  GCGGAGAGCGCTCCCCAGCTCAGACCTGGGGCCCTACCTCCCTACAGACAGGCCAA 123
          |||

```

Db 17974 GCGTTGAATGTCACCAAGCTCCACCTTGGCAGCCAGCGTCCGCGACAGCCTCAGGCGCG 17915
Qy 124 GGTAACTCTGAAGCAATCAGCGAGTGAAGGGGACAGTGCCTCCCGACGAGCCCTCAG 183
Db 17914 CGTCACATGTGCGGGGCTGCGCGTGGCGGGGACAGTGCCTCGGCTCGGGCGA 17855
Qy 184 GCGCGCTGGCGCCCACTGCC 204
Db 17854 GCGCGCGGTGCCACATGTC 17834

RESULT 11

US-09-949-016-12915/c
; Sequence 12915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12915
; LENGTH: 40546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12915

Query Match 6.2%; Score 37; DB 4; Length 40546;
Best Local Similarity 53.9%; Pred. No. 0.93;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 64 GCGGAGAGGCTCCCGACGCTCAGACCTGGGGCCCTACTCTCCTACACAGAGCCAA 123
Db 17974 GCGTTGAATGTCACCAAGCTCCACCTTGGCAGCCAGCGTCCGCGACAGCCTCAGGCGCG 17915
Qy 124 GGTAACTCTGAAGCAATCAGCGAGTGAAGGGGACAGTGCCTCCCGACGAGCCTCAG 183
Db 17914 CGTCACATGTGCGGGGCTGCGCGTGGCGGGGACAGTGCCTCGGCTCGGGCGA 17855
Qy 184 GCGCGCTGGCGCCCACTGCC 204
Db 17854 GCGCGCGGTGCCACATGTC 17834

RESULT 12

US-09-949-016-16359
; Sequence 16359, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16359

; LENGTH: 12787
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16359

Query Match 6.1%; Score 36.2; DB 4; Length 12787;
Best Local Similarity 51.6%; Pred. No. 0.88;
Matches 83; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 61 CCTCGGAGAGGCTCCCGACGCTCAGACCTGGGGCCCTACTCTCCTACACAGAGCCA 120
Db 9187 CCTCCCAAGCCCTGCTCTGSCCTCCCTTGTGAGTACTCTCCCAAGCCCGCTGCA 9246
Qy 121 CAAGGTAATCTCTGAAGCAATCAGCGAGTGAAGGGGACAGTGCCTCCCGACGAGCCCT 180
Db 9247 TTCCACAGGCCAAAGCCCTAGTGACAGTTCTTAGGGGACAGGACAGACTAGGGGGGCC 9306
Qy 181 CAGGCGCGCTGGCGCCCACTGCCAGCCCTGGCCCTTTTGC 221
Db 9307 CAGAGGCCACTAGAGAAACCTGCAGGTGCTGCGCCATCTGGC 9347

RESULT 13

US-09-949-016-14869/c
; Sequence 14869, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14869
; LENGTH: 15141
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14869

Query Match 6.1%; Score 36.2; DB 4; Length 15141;
Best Local Similarity 50.9%; Pred. No. 0.97;
Matches 86; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 217 TTTGCTACAGATCCCGCTTTTCATCTTTATGAGAGATCCTCCCTGCTGTCGATCC 276
Db 11806 TATGGCACCTGGCTGGGTTTTTTTGTGCTTTGCGCAATCTCTTAATCTTGGGATCC 11747
Qy 277 TCCAGTGGGTATTTCTCTTTTGACACACAGAGAGCCAGCACCACCATGAGTTGTGACAAA 336
Db 11746 TCCAGAGGGAAGGTCTTCTGGCTTGGCCCTAGGGGCAAGAGATGCTGATGTAATAA 11687
Qy 337 TCACACAAACCCCAAGTCCTCTTTCAGGCGCTTCAACCACTATCTCA 385
Db 11686 TCACATGGCTACCATGTACAGAGGACACCACTCCATGAGGGTCTCA 11638

RESULT 14

US-09-949-016-13086/c
; Sequence 13086, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13086

;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13086
;; LENGTH: 17740
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13086

Query Match 6.1%; Score 36.2; DB 4; Length 17740;
Best Local Similarity 50.9%; Pred. No. 1.1;
Matches 86; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 217 TTGCTACCATCCCGCTTTCATCTTTATGAGAATCCTCCCTGCTGTCGATCC 276
Db 12004 TATGCACCTGGCTGGCGTCTTTTGTGCTTTGCAGCAATCTCCTTAATCTGGGATCC 11945
QY 277 TCCAGTGGGTATTTCTCTTTTGACACAGACAGAGCCACCATGAGTTGTGACAAA 336
Db 11944 TCCACAGGAGGCTCTCTGGCTTGGCCCTAGGGGAGAAAGATGCTGATGTGAATAA 11885
QY 337 TCACACAAACCCCAAGTCTCTCTGCGGCTTCAACCACTATCTCA 385
Db 11884 TCACCATGGCTACCATGTACAGAGACACCACTCCAAATGAGGGTCTCA 11836

RESULT 15
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)863-4109
; INFORMATION FOR SEQ ID NO: 14:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7218 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; CLONE: pTZgpt-F1s
US-08-232-463-14
Query Match 6.0%; Score 36; DB 1; Length 7218;
Best Local Similarity 3.8%; Pred. No. 0.74;
Matches 9; Conservative 138; Mismatches 93; Indels 0; Gaps 0;
QY 162 CTGCCCCACGCGCAGCCCTCAGGGCCGCTGCCCCACCTGCAGCCCTGGCCCTTTTGC 221
Db 1212 YY 1271
QY 222 TACCATGATCCCGCTTTTCATCTTTATGAGAAGATCCTCCTGCTGCTCGATCCTCAG 281
Db 1272 YY 1331
QY 282 TGGGTATTTCTCTTTTGACACAGACAGAGCCAGCCAGCCATGAGTTGTGACAAATCAAC 341
Db 1332 YY 1391
QY 342 ACATACCCCAAGTCTCTCTGCGGCTTCAACCACTATCTCAGTCAATGGCTTCCAT 401
Db 1392 YY 1451

Search completed: November 12, 2005, 05:00:03
Job time : 176 secs

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OM nucleic - nucleic search, using sw model

Run on: November 12, 2005, 03:53:03 ; Search time 738 Seconds
(without alignments)
6678.607 Million cell updates/sec

Title: US-09-508-832-9

Perfect score: 596

Sequence: 1 atggcaagcaacctctga.....ctgggtggagatgcattg 596

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314	52.7	536	10	US-09-918-995-31159
2	292.4	49.1	826	20	US-10-755-889-15
3	276	46.3	442	24	US-10-450-783-1154
4	237	39.8	403	10	US-09-918-995-36495
5	110	18.5	455	14	US-10-027-632-75254

6	110	18.5	455	14	US-10-027-632-313542	Sequence 313542, A
7	110	18.5	455	18	US-10-027-632-75254	Sequence 75254, A
8	110	18.5	455	18	US-10-027-632-313542	Sequence 313542, A
9	105.2	17.7	199	15	US-10-092-750-72	Sequence 72, Appl
10	98.8	16.6	105	15	US-10-092-750-153	Sequence 153, Appl
11	60	10.1	60	10	US-09-908-975-13260	Sequence 13260, A
C 12	41.4	6.9	653	15	US-10-184-644-402	Sequence 402, App
C 13	41.4	6.9	653	15	US-10-184-634-402	Sequence 402, App
C 14	41	6.9	65	10	US-09-908-975-2414	Sequence 2414, App
C 15	38.6	6.5	55001	18	US-10-160-497-4	Sequence 4, Appli
C 16	38.6	6.5	55001	18	US-10-348-750-4	Sequence 4, Appli
C 17	38.6	6.5	55001	22	US-10-391-147-4	Sequence 4, Appli
C 18	38.4	6.4	1978	19	US-10-425-114-3109	Sequence 3109, App
C 19	38.4	6.4	2233	21	US-10-425-115-182927	Sequence 182927, A
C 20	37	6.2	410	9	US-09-960-352-11496	Sequence 11496, A
C 21	37	6.2	615	17	US-10-029-386-24080	Sequence 24080, A
C 22	37	6.2	2107	9	US-09-981-353-49	Sequence 49, Appl
C 23	37	6.2	2110	18	US-10-172-118-1846	Sequence 1846, App
C 24	37	6.2	2110	19	US-10-342-887-1846	Sequence 1846, App
C 25	37	6.2	2110	20	US-10-717-597-35	Sequence 35, Appl
C 26	37	6.2	2110	23	US-10-727-100-382	Sequence 382, App
C 27	37	6.2	4047	9	US-09-752-639-1	Sequence 1, Appli
C 28	37	6.2	4047	9	US-09-752-639-147	Sequence 147, App
C 29	37	6.2	4047	9	US-09-984-138-1	Sequence 1, Appli
C 30	37	6.2	4047	9	US-09-984-138-147	Sequence 147, App
C 31	37	6.2	4047	22	US-10-967-092-1	Sequence 1, Appli
C 32	37	6.2	4047	22	US-10-967-092-147	Sequence 147, App
C 33	37	6.2	4047	26	US-11-011-500-1	Sequence 1, Appli
C 34	37	6.2	4047	26	US-11-011-500-147	Sequence 147, App
C 35	37	6.2	4047	26	US-11-012-047-1	Sequence 1, Appli
C 36	37	6.2	4047	26	US-11-012-047-147	Sequence 147, App
C 37	36.8	6.2	480	9	US-09-864-761-1601	Sequence 1601, App
C 38	36.8	6.2	680	20	US-10-437-963-18984	Sequence 18984, A
C 39	36.6	6.1	65	10	US-09-908-975-28707	Sequence 28707, A
C 40	36.4	6.1	563	13	US-09-925-065A-810499	Sequence 810499, A
C 41	36.4	6.1	1318	14	US-10-027-632-84180	Sequence 84180, A
C 42	36.4	6.1	1318	18	US-10-027-632-84180	Sequence 84180, A
C 43	36	6.0	5487	16	US-10-156-761-2499	Sequence 2499, App
C 44	36	6.0	9025608	16	US-10-156-761-1	Sequence 1, Appli
C 45	35.8	6.0	569	9	US-09-864-761-9341	Sequence 9341, App

ALIGNMENTS

RESULT 1
US-09-918-995-31159
; Sequence 31159, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31159
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(536)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31159

Query Match 52.7%; Score 314; DB 10; Length 536;
Best Local Similarity 100.0%; Pred. No. 6e-98; Indels 0;
Matches 314; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ATGGCAAGACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAGGTAGACAATTGCAG 60
DB 223 ATGGCAAGACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAGGTAGACAATTGCAG 282
QY 61 CTGCGGAGAGGCTTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGAGCCA 120
DB 293 CTGCGGAGAGGCTTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGAGCCA 342
QY 121 CAAGTAATCTGAAAGGAATCAACGAGGTGAAGGGGACAGTGGCCCCCAGCGAGCCCT 180
DB 343 CAAGTAATCTGAAAGGAATCAACGAGGTGAAGGGGACAGTGGCCCCCAGCGAGCCCT 402
QY 181 CAGGCGCGCTGGCCCCACCTCCAGCCCTGGCCCTTTTGTACAGATCCCGCTTTTC 240
DB 403 CAGGCGCGCTGGCCCCACCTCCAGCCCTGGCCCTTTTGTACAGATCCCGCTTTTC 462
QY 241 ATCTTTATGAGAAGATCTCCCTGCTGCTCGATCTCCAGTGGGTATTTCTTTTGAC 300
DB 463 ATCTTTATGAGAAGATCTCCCTGCTGCTCGATCTCCAGTGGGTATTTCTTTTGAC 522
QY 301 ACAGACAGAGGCC 314
DB 523 ACAGACAGAGGCC 536

RESULT 2

US-10-755-889-15
; Sequence 15, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-15

Query Match 49.1%; Score 292.4; DB 20; Length 826;
Best Local Similarity 99.7%; Pred. No. 2.4e-90;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 303 AGACAGAGCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTTTG 362
DB 123 AGACAGAGCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTTTG 182
QY 363 CAGGCTTCAACCACTATCTAGTCAATGGTTCCATGAGGAGGCTGAACCTGCAGA 422
DB 183 CAGGCTTCAACCACTATCTAGTCAATGGTTCCATGAGGAGGCTGAACCTGCAGA 242
QY 423 TATGCGCCAGAGATGATGATCGCCCAAGTTTGGCGCTATCGGAGACGAGTTTAAACGC 482
DB 243 TATGCGCCAGAGATGATGATCGCCCAAGTTTGGCGCTATCGGAGACGAGTTTAAACGC 302
QY 483 TTACTATGCAAGAGGGTATTTTGAATAATTACCAAGCAGCGGAGACCAACCAAGAT 542
DB 303 TTACTATGCAAGAGGGTATTTTGAATAATTACCAAGCAGCGGAGACCAACCAAGAT 362
QY 543 GGTATCTTACGACTGTACGTTACATTTCCGCTGGTGTGGAGATGCAATG 596
DB 363 GGTATCTTACGACTGTACGTTACATTTCCGCTGGTGTGGAGATGCAATG 416

RESULT 3

US-10-450-763-1154
; Sequence 1154, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CI33/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 1154
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (167)-(442)
; OTHER INFORMATION: 100% homologous to Homo sapiens BimEL, accession number
; OTHER INFORMATION: AF032457, Smith-Waterman Score=497.
US-10-450-763-1154

Query Match 46.3%; Score 276; DB 24; Length 442;
Best Local Similarity 100.0%; Pred. No. 9e-85;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAGGTAGACAATTGCAG 60
DB 167 ATGCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAGGTAGACAATTGCAG 226
QY 61 CTGCGGAGAGGCTTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGAGCCA 120
DB 227 CTGCGGAGAGGCTTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGAGCCA 286
QY 121 CAAGTAATCTGAAAGGAATCAACGAGGTGAAGGGGACAGTGGCCCCCAGCGAGCCCT 180
DB 287 CAAGTAATCTGAAAGGAATCAACGAGGTGAAGGGGACAGTGGCCCCCAGCGAGCCCT 346
QY 181 CAGGCGCGCTGGCCCCACCTGCGAGCCCTGGCCCTTTTGTACAGATCCCGCTTTTC 240
DB 347 CAGGCGCGCTGGCCCCACCTGCGAGCCCTGGCCCTTTTGTACAGATCCCGCTTTTC 406
QY 241 ATCTTTATGAGAGATCTCCCTGCTGCTCGATCC 276
DB 407 ATCTTTATGAGAGATCTCCCTGCTGCTCGATCC 442

RESULT 4

US-09-918-995-36495
; Sequence 36495, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36495
; LENGTH: 403
; TYPE: DNA

ORGANISM: Homo sapiens
US-09-918-995-36495

Query Match 39.8%; Score 237; DB 10; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.1e-71; Mismatches 0; Indels 0; Gaps 0;
Matches 237; Conservative 0;

QY 1 ATGGCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAAGGTAGACAATTGCAG 60
Db |||||
167 ATGGCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAAGGTAGACAATTGCAG 226
QY 61 CCTGGGAGAGGCTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGGCA 120
Db |||||
227 CCTGGGAGAGGCTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGGCA 286
QY 121 CAAGGTAACTCTGAAGGAATCAGCGAGTGAAGGGGACAGCTGCCCCCAGCGCCCT 180
Db |||||
287 CAAGGTAACTCTGAAGGATCAGCGAGTGAAGGGGACAGCTGCCCCCAGCGCCCT 346
QY 181 CAGGGCCCGCTGGCCCCACCTGCCAGCCCTGGCCCTTTTGCTTACAGATCCCGCTT 237
Db |||||
347 CAGGGCCCGCTGGCCCCACCTGCCAGCCCTGGCCCTTTTGCTTACAGATCCCGCTT 403

RESULT 5
US-10-027-632-75254
; Sequence 75254, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75254
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75254

Query Match 18.5%; Score 110; DB 14; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 453
Db |||||
79 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 138
QY 454 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 513
Db |||||
139 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 198
QY 514 TACCAAGC 521
Db |||||
199 TTACCCGC 206

RESULT 7
US-10-027-632-75254
; Sequence 75254, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

Query Match 18.5%; Score 110; DB 14; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 453
Db |||||
79 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 138
QY 454 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 513
Db |||||
139 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 198
QY 514 TACCAAGC 521
Db |||||
199 TTACCCGC 206

RESULT 6
US-10-027-632-313542
; Sequence 313542, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313542
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-313542

Query Match 18.5%; Score 110; DB 14; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 453
Db |||||
79 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 138
QY 454 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 513
Db |||||
139 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 198
QY 514 TACCAAGC 521
Db |||||
199 TTACCCGC 206

RESULT 7
US-10-027-632-75254
; Sequence 75254, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

Query Match 18.5%; Score 110; DB 14; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 453
Db |||||
79 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 138
QY 454 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 513
Db |||||
139 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 198
QY 514 TACCAAGC 521
Db |||||
199 TTACCCGC 206

RESULT 7
US-10-027-632-75254
; Sequence 75254, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

Query Match 18.5%; Score 110; DB 14; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 453
Db |||||
79 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCAGAGATATGATCGCCCAAGAG 138
QY 454 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 513
Db |||||
139 TTGCGCGTATCGGAGACAGTTTAACTTACTATGCAAGAGGGTATTTTGAATAT 198
QY 514 TACCAAGC 521
Db |||||
199 TTACCCGC 206

;
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75254
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75254

Query Match 18.5%; Score 110; DB 18; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCCATGAGCAGGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 453
Db 79 GCTTCCATGAGCAGGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 138

QY 454 TTGCGCGTATCGGAGACAGTTTAAACGCTTACTATGCAAGAGGGTATTTTGAATAAT 513
Db 139 TTGCGCGTATCGGAGACAGTTTAAACGCTTACTATGCAAGAGGGTATTTTGAATAAT 198

QY 514 TACCAAGC 521
Db 199 TTACCCGC 206

RESULT 8
US-10-027-632-313542
; Sequence 313542, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313542
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-313542

Query Match 18.5%; Score 110; DB 18; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCCATGAGCAGGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 453
Db 79 GCTTCCATGAGCAGGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 138

QY 454 TTGCGCGTATCGGAGACAGTTTAAACGCTTACTATGCAAGAGGGTATTTTGAATAAT 513
Db 139 TTGCGCGTATCGGAGACAGTTTAAACGCTTACTATGCAAGAGGGTATTTTGAATAAT 198

QY 514 TACCAAGC 521
Db 199 TTACCCGC 206

RESULT 9
US-10-092-750-72
; Sequence 72, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XL
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-750-72

Query Match 17.7%; Score 105.2; DB 15; Length 199;
Best Local Similarity 89.7%; Pred. No. 1.5e-25;
Matches 113; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 374 ACCACTATCTCAGTCAATGCTTCCATGAGCAGGCTGAACCTGCAGATATGCGCCCAAG 433
Db 34 ACAATCTTACTTCAATGCTTCCATGAGCAGGCTGAACCTGCAGATATGCGCCCAAG 93

QY 434 AGATATGATGCGCCCAAGAGTTGCGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAA 493
Db 94 AGATATGATGCGCCCAAGAGTTGCGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAA 153

QY 494 GAGAGG 499
Db 154 GAGAGG 159

RESULT 10
US-10-092-750-153
; Sequence 153, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XL
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-750-153

Query Match 16.6%; Score 98.8; DB 15; Length 105;
Best Local Similarity 98.0%; Pred. No. 1.9e-23;
Matches 100; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 394 GCTTCCATGAGCAGGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 453
Db 1 GCTTCCATGAGCAGGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 60

Qy 454 TTGCGGGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGG 495
|||
Db 61 TTGCGGGCGTATTGGAGACGAGTTTAAACGCCCTACTATGCAAGG 102

RESULT 11

```

US-09-908-975-13260
; Sequence 13260, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY
; TITLE OF INVENTION: THAT POPULATE A TRAN
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908, 975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13260
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-13260

```

	Query Match	10.1%	Score 60;	DB 10;	Length 60;
	Best Local Similarity	100.0%	Prod. No. 4.6e-10;		
	Matches 60;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	445	GCCCAAGAGTTGCGGCGTATCGGAGACGAGTTAAACGCTTACTATGCAAGGAGGTATTT	504		
Db	1	GCCCAAGAGTTGCGGCGTATCGGAGACGAGTTAAACGCTTACTATGCAAGGAGGTATTT	60		

RESULT 12

```

US-10-184-644-402/c
; Sequence 402, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 402
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-402

```

Query Match 6.9%; Score 41.4; DB 15; Length 653;
Best Local Similarity 7.8%; Pred. No. 0.0038;

Matches	24, Conservative	111, Mismatches	171, Indels	0, Gaps	0,
Qy	93	GGCCCCCTACCTCCCTCAGACAGAGCCACAAAGGTAATCTCTGAAGGCAATCACGGAGGTGA	152		
Db	610	S.CT...M.A.MM..RSRBC.HH....SSSS..GYHM.M..AM.R..YH.MC..M.B..M	551		
Qy	153	AGGGGACAGTGGCCCCCAGCGAGCCCTCAGGGCCCGCTGGCCCCCAGCTGCCAGCCCTGG	212		
Db	550	DN..STSANT.B.RG.HMYN.H..NSSTYSDDYSSYSS..SYNYMDMDYMDCCSSSSSSS	491		
Qy	213	CCCTTTTGCTACCATGATCCCCGGCTTTTCATCTTATGAGAAGATCCCTCCCTGCTGTCTCG	272		
Db	490	SSBS..HTSSBSSSSASNYMM.M..MY.M.TSA..MMAM.M..M.T.M.Y...SM	431		
Qy	273	ATCCTCAGTGGGTATTCTCTTTTGACACAGACAGGAGGCCAGCCCATGAGTTGTGA	332		
Db	430	KRMD.M..TH.THM.A.H.T.TMMRS.TN..M.....CCY.B.A.G.RMYNTYDA.G	371		
Qy	333	CAAAATCAACAACAAACCCCAAGTCTCTCTTCCGAGGCCCTTCAACACCATCTCTCAGTGC	392		
Db	370	N..T...H..TMN.SCMATR.TCVTB.T.EN.MH...TMNR.NKTHBDCYB.RHBC.MB	311		
Qy	393	GGCTTC	398		
Db	310	GM.TWS	305		

RESULT 13

```

RES001 13
US-10-184-634-402/c
; Sequence 402, Application US/10184634
; Publication No. US2003068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 402
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-402

```

Query Match	6.9%	Score 41.4	DB 15	Length 653
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	Query match	Score	Score	DB	Length	8.55;
	Best Local Similarity	7.8%;	Pred. No.	0.0038;		
	Matches	24;	Conservative	111;	Mismatches	171;
					Indels	0;
					Gaps	0;
Qy	93	GGCCCCCTACCTCCTACAGACAGGCCACCAAGGTAACTCTGAAGGCAATACAGCGAGTGA	152			
Db	610	S.C.T...M.A.MM..RSRBC.HH....SSSS...GYHM.M..AM.R.YH.MC..M.B..M	551			
Qy	153	AGGGGACAGCTGCCCCACGGACGCCCTCAGGGCCGCTGCGCCACCTGCACGCCCTGG	212			
Db	550	DN...STANT.B.RG.HMYN.H..NSTYSSDIYSSYSS..SYNYMDMDYMDCSSSSSSS	491			
Qy	213	CCCTTTTGCTACCAGATCCCGCTTTTTCATCTTTATGAGAAGATCCCTCGTGTCTCG	272			
Db	490	SSBS.HTSSBSSSASMYMM.YM..M..MY.M.TSA..MMAM.M.M.T.M.Y...SM	431			
Qy	273	ATCCTCAGTGGGTATTCTCTTTTGACACAGACAGGAGGCCACACCCATGAGTGTGTA	332			

Db 430 KRMD.M..TH.THM.A.H.T.TMRRS.TN..M.....CCY.B.A.G.RMYTHYDA.G 371
QY 333 CAATCAACACAAACCCCAAGTCCTCTGCGAGCCCTTCAACCACTATCTCAGTGCAAT 392
Db 370 N.T...H..TMN.SMATR.TCYTB.T.BN.MH...TMNR.NKTHBDYCEM.RHBC.MB 311
QY 393 GCGTTC 398
Db 310 GM.TWS 305

RESULT 14

US-09-908-975-2414
; Sequence 2414, Application US/09908975
; Publication NO. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2414
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-908-975-2414

Query Match 6.9%; Score 41; DB 10; Length 65;
Best Local Similarity 76.9%; Pred. No. 0.0019;
Matches 50; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 432 ACAGATATCGATCGCCCAAGATCGCGGTATCGGAGACGAGTTTAAAGCTTACTATGC 491
Db 1 ACAGATACCGATCGCACAGGAGTCGCGGATCGGAGACGAGTTCAATGAGACTTACAC 60
QY 492 AAGGA 496
Db 61 GAGGA 65

RESULT 15

US-10-160-497-4/c
; Sequence 4, Application US/10160497
; Publication No. US20030224513A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH1 EXPRESSION
; FILE REFERENCE: RTS-0386
; CURRENT APPLICATION NUMBER: US/10/160,497
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 4
; LENGTH: 55001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-160-497-4

Query Match 6.5%; Score 38.6; DB 18; Length 55001;

Best Local Similarity 51.4%; Pred. No. 0.25;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 61 CCTGCGGAGAGCCCTTCCCACTCAGACTCAGCTGGGGCCCTTACTCTCCTTACAGACAGGCCA 120
Db 12959 CCTCCCCACAGAGCCCCCAGTCCCTCCCAAGAGCCCCCAGTCCCTCCCCACAGAGCCC 12900
QY 121 CAAGGTAATCCTGAGGCAATCAGGAGGTGAAGGGGACAGTGCCTCCCAAGAGCCCCCAGGAGCCCT 180
Db 12899 CCCAGTCCCTTCCCAACAGAGCCCCCGAGTCCCTCCCAAGAGCCCCCAGTCCCTCCCCA 12840
QY 181 CAGGGCCCGCTGGCCCCCACCTGCCAGCCCTGGCCCTTTTGTGTACAGATCCCC 233
Db 12839 CAGAGCCCCCGAGTCCCTCCCCACAGAGCCCGAGTCCCTCCCCACAGAGCCCC 12787

Search completed: November 12, 2005, 06:38:21
Job time : 745 secs